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Description A collection of various R functions for the purpose of Luminescence dating data analysis. This includes, amongst others, data import, export, application of age models, curve deconvolution, sequence analysis and plotting of equivalent dose distributions.

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Depends R (>= 3.1.2), utils

Imports methods, XML, shape, rgl, matrixStats, raster, sp, zoo, bbmle, data.table, Rcpp (>= 0.11.4), parallel

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Collate Analyse_SAR.OSLdata.R analyse_SAR.CWOSL.R analyse_SAR.TL.R analyse_IRSAR.RF.R CW2pLM.R CW2pLMi.R CW2pHMi.R CW2pPMi.R calc_FadingCorr.R calc_FuchsLang2001.R calc_OSLLxTxRatio.R calc_TLLxTxRatio.R Second2Gray.R fit_LMCurve.R fit_CWCurve.R plot_Risoe.BINfileData.R plot_KDE.R plot_GrowthCurve.R plot_Histogram.R plot_RadialPlot.R plot_RLum.R plot_RLum.Analysis.R plot_RLum.Data.Curve.R readBIN2R.R RisoeBINfileData-class.R Risoe.BINfileData2RLum.Analysis.R RLum-class.R RLum.Data-class.R RLum.Data.Curve-class.R RLum.Analysis-class.R RLum.Results-class.R calc_CentralDose.R calc_FiniteMixture.R calc_MinDose.R calc_CommonDose.R calc_CosmicDoseRate.R merge_Risoe.BINfileData.R writeR2BIN.R Risoe.BINfileData2RLum.Data.Curve.R calc_HomogeneityTest.R

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`Luminescence-package` *Comprehensive Luminescence Dating Data Analysis*

Description

A collection of various R functions for the purpose of Luminescence dating data analysis. This includes, amongst others, data import, export, application of age models, curve deconvolution, sequence analysis and plotting of equivalent dose distributions.

Details

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`analyse_IRSAR.RF` *Analyse IRSAR RF measurements*

Description

Function to analyse IRSAR RF measurements on K-feldspar samples, performed using the protocol according to Erfurt et al. (2003)

Usage

```
analyse_IRSAR.RF(object, sequence.structure = c("NATURAL", "REGENERATED"),
    method = "FIT", rejection.criteria, fit.range.min, fit.range.max,
    fit.trace = FALSE, fit.MC.runs = 10, slide.MC.runs = 10,
   slide.outlier.rm = FALSE, slide.trend.corr = FALSE, slide.show.density = TRUE,
    plot = TRUE, xlab.unit = "s", legend.pos, ...)
```

Arguments

`object`	`RLum.Analysis` (**required**): input object containing data for protocol analysis
`sequence.structure`	`vector character` (with default): specifies the general sequence structure. Allowed steps are `NATURAL`, `REGENERATED`. In addition any other character is allowed in the sequence structure; such curves will be ignored.
`method`	`character` (with default): setting method applied for the data analysis. Possible options are `"FIT"` or `"SLIDE"`.
`rejection.criteria`	`list (with default)`: set rejection criteria for, see details for more information **Currently without usage!**
`fit.range.min`	`integer` (optional): set the minimum channel range for signal fitting and sliding. Usually the entire data set is used for curve fitting, but there might be reasons to limit the channels used for fitting. Note: This option also limits the values used for natural signal calculation.
`fit.range.max`	`integer` (optional): set maximum channel range for signal fitting and sliding. Usually the entire data set is used for curve fitting, but there might be reasons to limit the channels used for fitting.

`fit.trace`	`logical` (with default): trace fitting (for debugging use)
`fit.MC.runs`	`numeric` (with default): set number of Monte Carlo runs for start parameter estimation. Note: Large values will significantly increase the calculation time.
`slide.MC.runs`	`integer` (with default): set number of Monte Carlo runs error calculation Note: Large values will significantly increase the calculation time.
`slide.outlier.rm`	`logical` (with default): enable or disable outlier removal. Outliers are removed from the natural signal curve only.
`slide.trend.corr`	`logical` (with default): enable or disable trend correction. If `TRUE`, the sliding is applied to a previously trend corrected data set.
`slide.show.density`	`logical` (with default): enable or disable KDE for MC runs. If `FALSE`, the final values are indicated with triangles.
`plot`	`logical` (with default): plot output (`TRUE` or `FALSE`)
`xlab.unit`	`character` (with default): set unit for x-axis
`legend.pos`	`character` (with default): useful keywords are `bottomright`, `bottom`, `bottomleft`, `left`, `topleft`, `top`, `topright`, `right` and `center`. For further details see `legend`.
`...`	further arguments that will be passed to the plot output. Currently supported arguments are `main`, `xlab`, `ylab`, `xlim`, `ylim`, `log`

Details

The function performs an IRSAR analysis described for K-feldspar samples by Erfurt et al. (2003) assuming a negligible sensitivity change of the RF signal.
General Sequence Structure (according to Erfurt et al. (2003))

1. Measuring IR-RF intensity of the natural dose for a few seconds ($D_{natural}$)
2. Bleach the samples under solar conditions for at least 30 min without changing the geometry
3. Waiting for at least one hour
4. Regeneration of the IR-RF signal to at least the natural level
5. Fitting data with a stretched exponential function
6. Calculate the the palaeodose D_e using the parameters from the fitting

Function Used For The Fitting (according to Erfurt et al. (2003))

$$\phi(D) = \phi_0 - \Delta\phi(1 - exp(-\lambda * D))^{\beta}$$

with $\phi(D)$ the dose dependent IR-RF flux, ϕ_0 the inital IR-RF flux, $\Delta\phi$ the dose dependent change of the IR-RF flux, λ the exponential parameter, D the dose and β the dispersive factor.

To obtain the palaeodose D_e the function is changed to:

$$D_e = ln(-(\phi(D) - \phi_0)/(-\lambda * \phi)^{1/\beta} + 1)/ - \lambda$$

The fitting is done using the `port` algorithm of the `nls` function.

Two methods are supported to obtain the De:

`method = "FIT"`

The principle is described above and follows the orignal suggestions from Erfurt et al., 2003.

`method = "SLIDE"`

For this method the natural curve is slided along the x-axis until congruence with the regenerated curve is reached. Instead of fitting this allows to work with the original data without the need of any physical model. This approach was introduced for RF curves by Buylaert et al., 2012 and Lapp et al., 2012.

Here the sliding is done by searching for the minimum of the residual squares.

$$min(\Sigma(RF.reg_{k.i} - RF.nat_{k.i})^2)$$

for

$$k = t.0 + i, ..., t.max + i$$

Correction for outliers (`slide.outlier.rm = TRUE`)

By using `method = "SLIDE"` and setting the argument `slide.outlier.rm = TRUE` an automatic outlier removal can be applied to the natural curve. Outliers may be observed also on the regenerative curve, but here the impact of single outliers on the curve adjustment (sliding) is considered as negligible.
The applied outlier removal algorithm consists of three steps:

(a) Input data are smoothed using the function `rollmedian`. Value `k` for the rolling window is fixed to 11. Therefore, the natural curve needs to comprise at least of 33 values, otherwise outlier removal is rejected.

(b) To subsequently remove outliers, code blocks from the function `apply_CosmicRayRemoval` were recycled, therefore in general the outlier correction works as described by Pych (2003). In contrast, here no sigma clipping before constructing the histograms is applied.

(c) Outliers are marked in the data set and visualised in the graphical output. The subsequent adjustement of both curves (natural and regenerative) is done without outliers, whereas the sliding itself is done with the entire data set.

Trend correction (`slide.trend.corr = TRUE`)

This option allows for correcting any linear trend in the natural curve in comparison to the regenerative curve. The trend correction is based on regression analysis of the residuals from the slided curve. The corrected De is obtained by sliding the trend corrected values (again) along the regenerative data curve. This correction is driven by the idea that the rediduals from the regenerative and the natural curve should be free of any trend, as long as they are comparable.

Error estimation

For `method = "FIT"` the asymmetric error range is taken from the standard deviation of the natural signal.

For `method = "SLIDE"` an beta-version of an error estimation based on boostrapping is implemented, however, this needs further documentation.

Value

A plot (optional) and an `RLum.Results` object is returned containing the following elements:

`De.values`	`data.frame` containing De-values with error (gray dashed lines in the plot) and further parameters. Corrected De values are only provided for the method `"SLIDE"`, provided the trend correction is applied.
`fit`	`nls` `nlsModel` object

Note: The output (`De.values`) should be accessed using the function `get_RLum.Results`

Function version

0.3.1 (2015-03-23 13:07:08)

Note

This function assumes that there is no sensitivity change during the measurements (natural vs. regenerated signal), which is in contrast to the findings from Buylaert et al. (2012).

Please note that `method = "FIT"` has beta status and was not properly tested yet!

Author(s)

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References

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Trautmann, T., Krbetschek, M.R., Dietrich, A., Stolz, W., 1999. Feldspar radioluminescence: a new dating method and its physical background. Journal of Luminescence 85, 45-58.

Trautmann, T., Krbetschek, M.R., Stolz, W., 2000. A systematic study of the radioluminescence properties of single feldspar grains. Radiation Measurements 32, 685-690.

See Also

RLum.Analysis, RLum.Results, get_RLum.Results, nls

Examples

```
##load data
data(ExampleData.RLum.Analysis, envir = environment())

##perform analysis
temp <- analyse_IRSAR.RF(object = IRSAR.RF.Data)
```

---

analyse_pIRIRSequence *Analyse post-IR IRSL sequences*

Description

The function performs an analysis of post-IR IRSL sequences including curve fitting on RLum.Analysis objects.

Usage

```
analyse_pIRIRSequence(object, signal.integral.min, signal.integral.max,
    background.integral.min, background.integral.max, dose.points,
    sequence.structure = c("TL", "IR50", "pIRIR225"), plot = TRUE,
    plot.single = FALSE, ...)
```

Arguments

object	RLum.Analysis(**required**): input object containing data for analysis
signal.integral.min	integer (**required**): lower bound of the signal integral. Provide this value as vector for different integration limits for the different IRSL curves.
signal.integral.max	integer (**required**): upper bound of the signal integral. Provide this value as vector for different integration limits for the different IRSL curves.
background.integral.min	integer (**required**): lower bound of the background integral. Provide this value as vector for different integration limits for the different IRSL curves.

`background.integral.max`
: integer (**required**): upper bound of the background integral. Provide this value as vector for different integration limits for the different IRSL curves.

`dose.points`
: numeric (optional): a numeric vector containing the dose points values. Using this argument overwrites dose point values in the signal curves.

`sequence.structure`
: vector character (with default): specifies the general sequence structure. Allowed values are `"TL"` and any `"IR"` combination (e.g., `"IR50"`,`"pIRIR225"`). Additionally a parameter `"EXCLUDE"` is allowed to exclude curves from the analysis (Note: If a preheat without PMT measurement is used, i.e. preheat as non TL, remove the TL step.)

`plot`
: logical (with default): enables or disables plot output.

`plot.single`
: logical (with default): single plot output (`TRUE/FALSE`) to allow for plotting the results in single plot windows. Requires `plot = TRUE`.

`...`
: further arguments that will be passed to the function `analyse_SAR.CWOSL` and `plot_GrowthCurve`

Details

To allow post-IR IRSL protocol (Thomsen et al., 2008) measurement analysis this function has been written as extended wrapper function for the function `analyse_SAR.CWOSL`, facilitating an entire sequence analysis in one run. With this, its functionality is strictly limited by the functionality of the function `analyse_SAR.CWOSL`.

Value

Plots (optional) and an `RLum.Results` object is returned containing the following elements:

`De.values`
: data.frame containing De-values, De-error and further parameters

.

`LnLxTnTx.values`
: data.frame of all calculated Lx/Tx values including signal, background counts and the dose points.

`rejection.criteria`
: data.frame with values that might by used as rejection criteria. NA is produced if no R0 dose point exists.

The output should be accessed using the function `get_RLum.Results`.

Function version

0.1.4 (2015-03-04 12:43:39)

Note

Best graphical output can be achieved by using the function `pdf` with the following options:
`pdf(file = "...", height = 15, width = 15)`

Author(s)

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R Luminescence Package Team

References

Murray, A.S., Wintle, A.G., 2000. Luminescence dating of quartz using an improved single-aliquot regenerative-dose protocol. Radiation Measurements 32, 57-73. doi:10.1016/S1350-4487(99)00253-X

Thomsen, K.J., Murray, A.S., Jain, M., Boetter-Jensen, L., 2008. Laboratory fading rates of various luminescence signals from feldspar-rich sediment extracts. Radiation Measurements 43, 1474-1486. doi:10.1016/j.radmeas.2008.06.002

See Also

analyse_SAR.CWOSL, calc_OSLLxTxRatio, plot_GrowthCurve, RLum.Analysis, RLum.Results get_RLum.Results

Examples

```
### NOTE: For this example existing example data are used. These data are non pIRIR data.
###
##(1) Compile example data set based on existing example data (SAR quartz measurement)
##(a) Load example data
data(ExampleData.BINfileData, envir = environment())

##(b) Transform the values from the first position in a RLum.Analysis object
object <- Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos=1)

##(c) Grep curves and exclude the last two (one TL and one IRSL)
object <- get_RLum.Analysis(object, record.id = c(-29,-30))

##(d) Define new sequence structure and set new RLum.Analysis object
sequence.structure  <- c(1,2,2,3,4,4)
sequence.structure <- as.vector(sapply(seq(0,length(object)-1,by = 4),
                                       function(x){sequence.structure + x}))

object <-  sapply(1:length(sequence.structure), function(x){

  object[[sequence.structure[x]]]

})

object <- set_RLum.Analysis(records = object, protocol = "pIRIR")

##(2) Perform pIRIR analysis (for this example with quartz OSL data!)
## Note: output as single plots to avoid problems with this example
results <- analyse_pIRIRSequence(object,
                              signal.integral.min = 1,
                              signal.integral.max = 2,
                              background.integral.min = 900,
                              background.integral.max = 1000,
                              fit.method = "EXP",
                              sequence.structure = c("TL", "pseudoIRSL1", "pseudoIRSL2"),
                              main = "Pseudo pIRIR data set based on quartz OSL",
                              plot.single = TRUE)


##(3) Perform pIRIR analysis (for this example with quartz OSL data!)
```

```
## Alternative for PDF output, uncomment and complete for usage
##
# pdf(file = "...", height = 15, width = 15)
#  results <- analyse_pIRIRSequence(object,
#         signal.integral.min = 1,
#         signal.integral.max = 2,
#         background.integral.min = 900,
#         background.integral.max = 1000,
#         fit.method = "EXP",
#         main = "Pseudo pIRIR data set based on quartz OSL")
#
#  dev.off()
```

`analyse_SAR.CWOSL` *Analyse SAR CW-OSL measurements*

Description

The function performs a SAR CW-OSL analysis on an `RLum.Analysis` object including growth curve fitting.

Usage

```
analyse_SAR.CWOSL(object, signal.integral.min, signal.integral.max,
    background.integral.min, background.integral.max, rejection.criteria,
    dose.points, mtext.outer, plot = TRUE, plot.single = FALSE,
    ...)
```

Arguments

`object`	`RLum.Analysis`(**required**): input object containing data for analysis
`signal.integral.min`	`integer` (**required**): lower bound of the signal integral
`signal.integral.max`	`integer` (**required**): upper bound of the signal integral
`background.integral.min`	`integer` (**required**): lower bound of the background integral
`background.integral.max`	`integer` (**required**): upper bound of the background integral
`rejection.criteria`	`list` (with default): provide list and set rejection criteria in percentage for further calculation. Allowed arguments are `recycling.ratio`, `recuperation.rate`, `palaeodose.error` and `exceed.max.regpoint = TRUE/FALS` e.g. `rejection.criteria = list(r` Per default all values are set to 10.
`dose.points`	`numeric` (optional): a numeric vector containg the dose points values Using this argument overwrites dose point values in the signal curves.
`mtext.outer`	`character` (optional): option to provide an outer margin mtext
`plot`	`logical` (with default): enables or disables plot output.

plot.single	logical (with default) or numeric (optional): single plot output (TRUE/FALSE) to allow for plotting the results in single plot windows. If a numerice vector is provided the plots can be selected individually, i.e. plot.single = c(1,2,3,4) will plot the TL and Lx, Tx curves but not the legend (5) or the growth curve (6), (7) and (8) belong to rejection criteria plots. Requires plot = TRUE.
...	further arguments that will be passed to the function plot_GrowthCurve

Details

The function performs an analysis for a standard SAR protocol measurements introduced by Murray and Wintle (2000) with CW-OSL curves. For the calculation of the Lx/Tx value the function calc_OSLLxTxRatio is used.

Working with IRSL data

The function was originally designed to work just for 'OSL' curves, following the principles of the SAR protocol. An IRSL measurement protocol may follow this procedure, e.g., post-IR IRSL protocol (Thomsen et al., 2008). Therefore this functions has been enhanced to work with IRSL data, however, the function is only capable of analysing curves that follow the SAR protocol structure, i.e., to analyse a post-IR IRSL protocol, curve data have to be pre-selected by the user to fit the standards of the SAR protocol, i.e., Lx,Tx,Lx,Tx and so on.

Example: Imagine the measurement contains pIRIR50 and pIRIR225 IRSL curves. Only one curve type can be analysed at the same time: The pIRIR50 curves or the pIRIR225 curves.

Supported rejection criteria

'recyling.ratio': calculated for every repeated regeneration dose point.

'recuperation.rate': recuperation rate calculated by comparing the Lx/Tx values of the zero regeneration point with the Ln/Tn value (the Lx/Tx ratio of the natural signal). For methodological background see Aitken and Smith (1988).

'palaeodose.error': set the allowed error for the De value, which per default should not exceed 10%.

Value

A plot (optional) and an RLum.Results object is returned containing the following elements:

De.values	data.frame containing De-values, De-error and further parameters
LnLxTnTx.values	data.frame of all calculated Lx/Tx values including signal, background counts and the dose points
rejection.criteria	data.frame with values that might by used as rejection criteria. NA is produced if no R0 dose point exists.
Formula	formula formula that have been used for the growth curve fitting

The output should be accessed using the function get_RLum.Results.

Function version

0.5.1 (2015-03-09 15:43:53)

Note

This function must not be mixed up with the function Analyse_SAR.OSLdata, which works with Risoe.BINfileData-class objects.

The function currently does only support 'OSL' or 'IRSL' data!

Author(s)

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R Luminescence Package Team

References

Aitken, M.J. and Smith, B.W., 1988. Optical dating: recuperation after bleaching. Quaternary Science Reviews 7, 387-393.

Duller, G., 2003. Distinguishing quartz and feldspar in single grain luminescence measurements. Radiation Measurements, 37 (2), 161-165.

Murray, A.S. and Wintle, A.G., 2000. Luminescence dating of quartz using an improved single-aliquot regenerative-dose protocol. Radiation Measurements 32, 57-73.

Thomsen, K.J., Murray, A.S., Jain, M., Boetter-Jensen, L., 2008. Laboratory fading rates of various luminescence signals from feldspar-rich sediment extracts. Radiation Measurements 43, 1474-1486. doi:10.1016/j.radmeas.2008.06.002

See Also

calc_OSLLxTxRatio, plot_GrowthCurve, RLum.Analysis, RLum.Results get_RLum.Results

Examples

```
##load data
##ExampleData.BINfileData contains two BINfileData objects
##CWOSL.SAR.Data and TL.SAR.Data
data(ExampleData.BINfileData, envir = environment())

##transform the values from the first position in a RLum.Analysis object
object <- Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos=1)

##perform SAR analysis
results <- analyse_SAR.CWOSL(object,
                  signal.integral.min = 1,
                  signal.integral.max = 2,
                  background.integral.min = 900,
                  background.integral.max = 1000,
                  log = "x",
                  fit.method = "EXP")
```

```
##show De results
get_RLum.Results(results)

##show LnTnLxTx table
get_RLum.Results(results, data.object = "LnLxTnTx.table")
```

`Analyse_SAR.OSLdata` *Analyse SAR CW-OSL measurements.*

Description

The function analyses SAR CW-OSL curve data and provides a summary of the measured data for every position. The output of the function is optimised for SAR OSL measurements on quartz.

Usage

```
Analyse_SAR.OSLdata(input.data, signal.integral, background.integral,
   position, run, set, dtype, keep.SEL = FALSE, info.measurement = "unkown measurement",
    log = "", output.plot = FALSE, output.plot.single = FALSE,
    cex.global = 1)
```

Arguments

`input.data`	Risoe.BINfileData-class (**required**): input data from a Risoe BIN file, produced by the function readBIN2R.
`signal.integral`	vector (**required**): channels used for the signal integral, e.g. `signal.integral=c(1:2)`
`background.integral`	vector (**required**): channels used for the background integral, e.g. `background.integral=c(85:100`
`position`	vector (optional): reader positions that want to be analysed (e.g. `position=c(1:48)`. Empty positions are automatically omitted. If no value is given all positions are analysed by default.
`run`	vector (optional): range of runs used for the analysis. If no value is given the range of the runs in the sequence is deduced from the Risoe.BINfileData object.
`set`	vector (optional): range of sets used for the analysis. If no value is given the range of the sets in the sequence is deduced from the `Risoe.BINfileData` object.
`dtype`	`character` (optional): allows to further limit the curves by their data type (`DTYPE`), e.g., `dtype = c("Natural", "Dose")` limits the curves to this two data types. By default all values are allowed. See Risoe.BINfileData-class for allowed data types.
`keep.SEL`	`logical` (default): option allowing to use the `SEL` element of the Risoe.BINfileData-class manually. NOTE: In this case any limitation provided by `run`, `set` and `dtype` are ignored!
`info.measurement`	character (with default): option to provide information about the measurement on the plot output (e.g. name of the BIN or BINX file).

`log` character (with default): a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic. See plot.default.

`output.plot` logical (with default): plot output (`TRUE/FALSE`)

`output.plot.single` logical (with default): single plot output (`TRUE/FALSE`) to allow for plotting the results in single plot windows. Requires `output.plot = TRUE`.

`cex.global` numeric (with default): global scaling factor.

Details

The function works only for standard SAR protocol measurements introduced by Murray and Wintle (2000) with CW-OSL curves. For the calculation of the Lx/Tx value the function calc_OSLLxTxRatio is used.

Provided rejection criteria

'recyling ratio': calculated for every repeated regeneration dose point.
'recuperation': recuperation rate calculated by comparing the Lx/Tx values of the zero regeneration point with the Ln/Tn value (the Lx/Tx ratio of the natural signal). For methodological background see Aitken and Smith (1988)

'IRSL/BOSL': the integrated counts (`signal.integral`) of an IRSL curve are compared to the integrated counts of the first regenerated dose point. It is assumed that IRSL curves got the same dose as the first regenerated dose point. **Note:** This is not the IR depletation ratio described by Duller (2003).

Value

A plot (optional) and list is returned containing the following elements:

`LnLxTnTx` data.frame of all calculated Lx/Tx values including signal, background counts and the dose points.

`RejectionCriteria` data.frame with values that might by used as rejection criteria. NA is produced if no R0 dose point exists.

`SARParameters` data.frame of additional measurement parameters obtained from the BIN file, e.g. preheat or read temperature (not valid for all types of measurements).

Function version

0.2.15 (2015-03-04 00:19:53)

Note

Rejection criteria are calculated but not considered during the analysis to discard values.

The development of this function will not be continued. We recommend to use the function analyse_SAR.CWOSL instead.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Margret C. Fuchs, AWI Potsdam (Germany), TU Bergakademie Freiberg (Germany)
R Luminescence Package Team

References

Aitken, M.J. and Smith, B.W., 1988. Optical dating: recuperation after bleaching. Quaternary Science Reviews 7, 387-393.

Duller, G., 2003. Distinguishing quartz and feldspar in single grain luminescence measurements. Radiation Measurements, 37 (2), 161-165.

Murray, A.S. and Wintle, A.G., 2000. Luminescence dating of quartz using an improved single-aliquot regenerative-dose protocol. Radiation Measurements 32, 57-73.

See Also

calc_OSLLxTxRatio, Risoe.BINfileData-class, readBIN2R

and for further analysis plot_GrowthCurve

Examples

```
##load data
data(ExampleData.BINfileData, envir = environment())

##analyse data
output <- Analyse_SAR.OSLdata(input.data = CWOSL.SAR.Data,
                              signal.integral = c(1:5),
                              background.integral = c(900:1000),
                              position = c(1:1),
                              output.plot = TRUE)

##combine results relevant for further analysis
output.SAR <- data.frame(Dose = output$LnLxTnTx[[1]]$Dose,
                         LxTx = output$LnLxTnTx[[1]]$LxTx,
                         LxTx.Error = output$LnLxTnTx[[1]]$LxTx.Error)
output.SAR
```

---

analyse_SAR.TL *Analyse SAR TL measurements*

Description

The function performs a SAR TL analysis on a RLum.Analysis object including growth curve fitting.

Usage

```
analyse_SAR.TL(object, object.background, signal.integral.min,
    signal.integral.max, sequence.structure = c("PREHEAT", "SIGNAL",
        "BACKGROUND"), rejection.criteria = list(recycling.ratio = 10,
        recuperation.rate = 10), log = "", ...)
```

Arguments

object	RLum.Analysis(**required**): input object containing data for analysis
object.background	currently not used
signal.integral.min	integer (**required**): requires the channel number for the lower signal integral bound (e.g. signal.integral.min = 100)
signal.integral.max	integer (**required**): requires the channel number for the upper signal integral bound (e.g. signal.integral.max = 200)
sequence.structure	vector character (with default): specifies the general sequence structure. Three steps are allowed ("PREHEAT", "SIGNAL", "BACKGROUND"), in addition a parameter "EXCLUDE". This allows excluding TL curves which are not relevant for the protocol analysis. (Note: None TL are removed by default)
rejection.criteria	list (with default): list containing rejection criteria in percentage for the calculation.
log	character (with default): a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic. See plot.default).
...	further arguments that will be passed to the function plot_GrowthCurve

Details

This function performs a SAR TL analysis on a set of curves. The SAR procedure in general is given by Murray and Wintle (2000). For the calculation of the Lx/Tx value the function calc_TLLxTxRatio is used.

Provided rejection criteria

'recyling.ratio': calculated for every repeated regeneration dose point.
'recuperation.rate': recuperation rate calculated by comparing the Lx/Tx values of the zero regeneration point with the Ln/Tn value (the Lx/Tx ratio of the natural signal). For methodological background see Aitken and Smith (1988)

Value

A plot (optional) and an RLum.Results object is returned containing the following elements:

De.values	data.frame containing De-values and further parameters
LnLxTnTx.values	data.frame of all calculated Lx/Tx values including signal, background counts and the dose points.
rejection.criteria	data.frame with values that might by used as rejection criteria. NA is produced if no R0 dose point exists.

note: the output should be accessed using the function get_RLum.Results

Function version

0.1.4 (2015-03-04 00:19:53)

Note

THIS IS A BETA VERSION

None TL curves will be removed from the input object without further warning.

Author(s)

Sebastian Kreutzer, Freiberg Instruments/JLU Giessen (Germany)
R Luminescence Package Team

References

Aitken, M.J. and Smith, B.W., 1988. Optical dating: recuperation after bleaching. Quaternary Science Reviews 7, 387-393.

Murray, A.S. and Wintle, A.G., 2000. Luminescence dating of quartz using an improved single-aliquot regenerative-dose protocol. Radiation Measurements 32, 57-73.

See Also

calc_TLLxTxRatio, plot_GrowthCurve, RLum.Analysis, RLum.Results get_RLum.Results

Examples

```
##load data
data(ExampleData.BINfileData, envir = environment())

##transform the values from the first position in a RLum.Analysis object
object <- Risoe.BINfileData2RLum.Analysis(TL.SAR.Data, pos=3)

##perform analysis
analyse_SAR.TL(object,
               signal.integral.min = 210,
               signal.integral.max = 220,
               log = "y",
               fit.method = "EXP OR LIN",
               sequence.structure = c("SIGNAL", "BACKGROUND"))
```

---

apply_CosmicRayRemoval

Function to remove cosmic rays from an RLum.Data.Spectrum S4 class object

---

Description

The function provides several methods for cosmic ray removal and spectrum smoothing for an RLum.Data.Spectrum S4 class object

Usage

```
apply_CosmicRayRemoval(object, method = "Pych", method.Pych.smoothing = 2,
    silent = FALSE, plot = FALSE, ...)
```

Arguments

object	RLum.Data.Spectrum (**required**): S4 object of class RLum.Data.Spectrum
method	character (with default): Defines method that is applied for cosmic ray removal. Allowed methods are smooth (smooth), smooth.spline (smooth.spline) and Pych (default). See details for further information.
method.Pych.smoothing	integer (with default): Smoothing parameter for cosmic ray removal according to Pych (2003). The value defines how many neighboring values in each frame are used for smoothing (e.g., 2 means that the two previous and two following values are used).
silent	logical (with default): Option to suppress terminal output.,
plot	logical (with default): If TRUE the histograms used for the cosmic-ray removal are returned as plot including the used threshold. Note: A separat plot is returned for each frame! Currently only for method = "Pych" a graphical output is provided.
...	further arguments and graphical parameters that will be passed to the smooth function.

Details

`method = "Pych"`

This method applies the cosmic-ray removal algorithm described by Pych (2003). Some aspects that are different to the publication:

- For interpolation between neighbouring values the median and not the mean is used.
- The number of breaks to construct the histogram is set to: `length(number.of.input.values)/2`

For further details see references below.

`method = "smooth"`

Method uses the function smooth to remove cosmic rays.

Arguments that can be passed are: kind, twiceit

`method = "smooth.spline"`
Method uses the function smooth.spline to remove cosmic rays.
Arguments that can be passed are: spar

How to combine methods?

Different methods can be combined by applying the method repeatedly to the dataset (see example).

Value

Returns same object as input (RLum.Data.Spectrum)

Function version

0.1.3 (2015-03-21 10:34:18)

Note

-

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France) R Luminescence Package Team

References

Pych, W., 2003. A Fast Algorithm for Cosmic-Ray Removal from Single Images. Astrophysics 116, 148-153. http://arxiv.org/pdf/astro-ph/0311290.pdf?origin=publication_detail

See Also

RLum.Data.Spectrum, smooth, smooth.spline, apply_CosmicRayRemoval

Examples

```
##(1) - use with your own data and combine (uncomment for usage)
## run two times the default method and smooth with another method
## your.spectrum <- apply_CosmicRayRemoval(your.spectrum, method = "Pych")
## your.spectrum <- apply_CosmicRayRemoval(your.spectrum, method = "Pych")
## your.spectrum <- apply_CosmicRayRemoval(your.spectrum, method = "smooth")
```

---

apply_EfficiencyCorrection

Function to apply spectral efficiency correction to RLum.Data.Spectrum S4 class objects

---

Description

The function allows spectral efficiency corrections for RLum.Data.Spectrum S4 class objects

Usage

```
apply_EfficiencyCorrection(object, spectral.efficiency)
```

Arguments

object	RLum.Data.Spectrum (**required**): S4 object of class RLum.Data.Spectrum
spectral.efficiency	data.frame (**required**): Data set containing wavelengths (x-column) and relative spectral response values (y-column) in percentage

Details

The efficiency correction is based on a spectral response dataset provided by the user. Usually the data set for the quantum efficiency is of lower resolution and values are interpolated for the required spectral resolution.

Value

Returns same object as input (RLum.Data.Spectrum)

Function version

0.1 (2015-03-04 00:19:53)

Note

Please note that the spectral efficiency data from the camera may not sufficiently correct for spectral efficiency of the entire optical system (e.g., spectrometer, camera ...).

This function has BETA status.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Johannes Friedrich, University of Bayreuth (Germany)
R Luminescence Package Team

References

-

See Also

RLum.Data.Spectrum

Examples

```
##(1) - use with your own data (uncomment for usage)
## spectral.efficiency <- read.csv("your data")
##
## your.spectrum <- apply_EfficiencyCorrection(your.spectrum, )
```

`BaseDataSet.CosmicDoseRate`

Base data set for cosmic dose rate calculation

Description

Collection of data from various sources needed for cosmic dose rate calculation

Usage

```
BaseDataSet.CosmicDoseRate
```

Format

`values.cosmic.Softcomp`:	data frame containing cosmic dose rates for shallow depths (< 167 g cm^-2) obtained using
`values.factor.Altitude`:	data frame containing altitude factors for adjusting geomagnetic field-change factors. Value
`values.par.FJH`:	data frame containing values for parameters F, J and H (read from Fig. 2 in Prescott & Hutt

$$Dc = D0 * (F + J * exp((altitude/1000)/H))$$

Version

0.1

Source

The following data were carefully read from figures in mentioned sources and used for fitting procedures. The derived expressions are used in the function `calc_CosmicDoseRate`.

values.cosmic.Softcomp

Program:	"AGE"
Reference:	Gruen (2009)
Fit:	Polynomials in the form of

For depths between 40-167 g cm^-2:

$$y = 2 * 10^-6 * x^2 - 0.0008 * x + 0.2535$$

(For depths <40 g cm^-2)

$$y = -6 * 10^-8 * x^3 + 2 * 10^-5 * x^2 - 0.0025 * x + 0.2969$$

values.factor.Altitude

Reference:	Prescott & Hutton (1994)
Page:	499
Figure:	1
Fit:	2-degree polynomial in the form of

$$y = -0.026 * x^2 + 0.6628 * x + 1.0435$$

values.par.FJH

Reference:	Prescott & Hutton (1994)
Page:	500
Figure:	2
Fits:	3-degree polynomials and linear fits

F (non-linear part, λ < 36.5 deg.):

$$y = -7 * 10^-7 * x^3 - 8 * 10^-5 * x^2 - 0.0009 * x + 0.3988$$

F (linear part, λ > 36.5 deg.):

$$y = -0.0001 * x + 0.2347$$

J (non-linear part, λ < 34 deg.):

$$y = 5 * 10^-6 * x^3 - 5 * 10^-5 * x^2 + 0.0026 * x + 0.5177$$

J (linear part, λ > 34 deg.):

$$y = 0.0005 * x + 0.7388$$

H (non-linear part, λ < 36 deg.):

$$y = -3 * 10^-6 * x^3 - 5 * 10^-5 * x^2 - 0.0031 * x + 4.398$$

H (linear part, λ > 36 deg.):

$$y = 0.0002 * x + 4.0914$$

References

Gruen, R., 2009. The "AGE" program for the calculation of luminescence age estimates. Ancient TL, 27, pp. 45-46.

Prescott, J.R., Hutton, J.T., 1988. Cosmic ray and gamma ray dosimetry for TL and ESR. Nuclear Tracks and Radiation Measurements, 14, pp. 223-227.

Prescott, J.R., Hutton, J.T., 1994. Cosmic ray contributions to dose rates for luminescence and ESR dating: large depths and long-term time variations. Radiation Measurements, 23, pp. 497-500.

Examples

```
##load data
data(BaseDataSet.CosmicDoseRate)
```

`calc_AliquotSize` *Estimate the amount of grains on an aliquot*

Description

Estimate the number of grains on an aliquot. Alternatively, the packing density of an aliquot is computed.

Usage

```
calc_AliquotSize(grain.size, sample.diameter, packing.density = 0.65,
    MC = TRUE, grains.counted, plot = TRUE, ...)
```

Arguments

`grain.size`	`numeric` (**required**): mean grain size (microns) or a range of grain sizes from which the mean grain size is computed (e.g. `c(100,200)`).
`sample.diameter`	`numeric` (**required**): diameter (mm) of the targeted area on the sample carrier.
`packing.density`	`numeric` (with default) empirical value for mean packing density. If `packing.density = "inf"` a hexagonal structure on an infinite plane with a packing density of $0.906\ldots$ is assumed.
`MC`	`logical` (optional): if `TRUE` the function performs a monte carlo simulation for estimating the amount of grains on the sample carrier and assumes random errors in grain size distribution and packing density. Requires a vector with min and max grain size for `grain.size`. For more information see details.
`grains.counted`	`numeric` (optional) grains counted on a sample carrier. If a non-zero positive integer is provided this function will calculate the packing density of the aliquot. If more than one value is provided the mean packing density and its standard deviation is calculated. Note that this overrides `packing.density`.
`plot`	`logical` (with default): plot output (`TRUE`/`FALSE`)
`...`	further arguments to pass (`main, xlab, MC.iter`).

Details

This function can be used to either estimate the number of grains on an aliquot or to compute the packing density depending on the the arguments provided.
The following function is used to estimate the number of grains `n`:

$$n = (\pi * x^2)/(\pi * y^2) * d$$

where `x` is the radius of the aliquot size (microns), `y` is the mean radius of the mineral grains (mm) and `d` is the packing density (value between 0 and 1).

Packing density

The default value for `packing.density` is 0.65, which is the mean of empirical values determined by Heer et al. (2012) and unpublished data from the Cologne luminescence laboratory. If `packing.density = "inf"` a maximum density of $\pi/\sqrt{12} = 0.9068\ldots$ is used. However, note

that this value is not appropriate as the standard preparation procedure of aliquots resembles a PECC ("Packing Equal Circles in a Circle") problem where the maximum packing density is asymptotic to about 0.87.

Monte Carlo simulation

The number of grains on an aliquot can be estimated by Monte Carlo simulation when setting `MC = TRUE`. Each of the parameters necessary to calculate `n` (`x`, `y`, `d`) are assumed to be normally distributed with means μ_x, μ_y, μ_d and standard deviations $\sigma_x, \sigma_y, \sigma_d$.

For the mean grain size random samples are taken first from $N(\mu_y, \sigma_y)$, where $\mu_y = mean.grain.size$ and $\sigma_y = (max.grain.size - min.grain.size)/4$ so that 95% of all grains are within the provided the grain size range. This effectively takes into account that after sieving the sample there is still a small chance of having grains smaller or larger than the used mesh sizes. For each random sample the mean grain size is calculated, from which random subsamples are drawn for the Monte Carlo simulation.

The packing density is assumed to be normally distributed with an empirically determined $\mu = 0.65$ (or provided value) and $\sigma = 0.18$. The normal distribution is truncated at `d = 0.87` as this is approximately the maximum packing density that can be achieved in PECC problem.

The sample diameter has $\mu = sample.diameter$ and $\sigma = 0.2$ to take into account variations in sample disc preparation (i.e. applying silicon spray to the disc). A lower truncation point at `x = 0.5` is used, which assumes that aliqouts with smaller sample diameters of 0.5 mm are discarded. Likewise, the normal distribution is truncated at 9.8 mm, which is the diameter of the sample disc.

For each random sample drawn from the normal distributions the amount of grains on the aliquot is calculated. By default, `10^5` iterations are used, but can be reduced/increased with `MC.iter` (see `...`). The results are visualised in a bar- and boxplot together with a statistical summary.

Value

Returns a terminal output. In addition an `RLum.Results` object is returned containing the following element:

`summary`	data.frame summary of all relevant calculation results.
`args`	list used arguments
`call`	call the function call
`MC`	list results of the Monte Carlo simulation

The output should be accessed using the function `get_RLum.Results`

Function version

0.31 (2015-03-04 00:19:53)

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team

References

Duller, G.A.T., 2008. Single-grain optical dating of Quaternary sediments: why aliquot size matters in luminescence dating. Boreas 37, 589-612.

Heer, A.J., Adamiec, G., Moska, P., 2012. How many grains are there on a single aliquot?. Ancient TL 30, 9-16.

Further reading

Chang, H.-C., Wang, L.-C., 2010. A simple proof of Thue's Theorem on Circle Packing. http://arxiv.org/pdf/1009.4322v1.pdf, 2013-09-13.

Graham, R.L., Lubachevsky, B.D., Nurmela, K.J., Oestergard, P.R.J., 1998. Dense packings of congruent circles in a circle. Discrete Mathematics 181, 139-154.

Huang, W., Ye, T., 2011. Global optimization method for finding dense packings of equal circles in a circle. European Journal of Operational Research 210, 474-481.

Examples

```
## Estimate the amount of grains on a small aliquot
calc_AliquotSize(grain.size = c(100,150), sample.diameter = 1)

## Calculate the mean packing density of large aliquots
calc_AliquotSize(grain.size = c(100,200), sample.diameter = 8,
                 grains.counted = c(2525,2312,2880))
```

---

calc_CentralDose — *Apply the central age model (CAM) after Galbraith et al. (1999) to a given De distribution*

Description

This function calculates the central dose and dispersion of the De distribution, their standard errors and the profile log likelihood function for sigma.

Usage

```
calc_CentralDose(data, sigmab, plot = TRUE, ...)
```

Arguments

data	RLum.Results or data.frame (**required**): for data.frame: two columns with De (data[,1]) and De error (values[,2])
sigmab	numeric (with default): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
plot	logical (with default): plot output
...	further arguments (trace, verbose).

Details

This function uses the equations of Galbraith et al. (1999, 358-359). The parameter `sigma` is estimated using the maximum likelihood approach. A detailed explanation on maximum likelihood estimation can be found in the appendix of Galbraith & Laslett (1993, 468-470)

Value

Returns a plot (optional) and terminal output. In addition an `RLum.Results` object is returned containing the following element:

`summary`	data.frame summary of all relevant model results.
`data`	data.frame original input data
`args`	list used arguments
`call`	call the function call
`profile`	data.frame the log likelihood profile for sigma

The output should be accessed using the function `get_RLum.Results`

Function version

1.3 (2015-03-04 13:35:16)

Author(s)

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2010

R Luminescence Package Team

References

Galbraith, R.F. & Laslett, G.M., 1993. Statistical models for mixed fission track ages. Nuclear Tracks Radiation Measurements 4, 459-470.

Galbraith, R.F., Roberts, R.G., Laslett, G.M., Yoshida, H. & Olley, J.M., 1999. Optical dating of single grains of quartz from Jinmium rock shelter, northern Australia. Part I: experimental design and statistical models. Archaeometry 41, 339-364.

Galbraith, R.F. & Roberts, R.G., 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: An overview and some recommendations. Quaternary Geochronology 11, 1-27.

Further reading

Arnold, L.J. & Roberts, R.G., 2009. Stochastic modelling of multi-grain equivalent dose (De) distributions: Implications for OSL dating of sediment mixtures. Quaternary Geochronology 4, 204-230.

Bailey, R.M. & Arnold, L.J., 2006. Statistical modelling of single grain quartz De distributions and an assessment of procedures for estimating burial dose. Quaternary Science Reviews 25, 2475-2502.

Cunningham, A.C. & Wallinga, J., 2012. Realizing the potential of fluvial archives using robust

OSL chronologies. Quaternary Geochronology 12, 98-106.

Rodnight, H., Duller, G.A.T., Wintle, A.G. & Tooth, S., 2006. Assessing the reproducibility and accuracy of optical dating of fluvial deposits. Quaternary Geochronology, 1 109-120.

Rodnight, H., 2008. How many equivalent dose values are needed to obtain a reproducible distribution?. Ancient TL 26, 3-10.

See Also

plot, calc_CommonDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MinDose

Examples

```
##load example data
data(ExampleData.DeValues, envir = environment())

##apply the central dose model
calc_CentralDose(ExampleData.DeValues$CA1)
```

---

calc_CommonDose — *Apply the (un-)logged common age model after Galbraith et al. (1999) to a given De distribution*

Description

Function to calculate the common dose of a De distribution.

Usage

```
calc_CommonDose(data, sigmab, log = TRUE, ...)
```

Arguments

data	RLum.Results or data.frame (**required**): for data.frame: two columns with De (data[,1]) and De error (values[,2])
sigmab	numeric (with default): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
log	logical (with default): fit the (un-)logged common age model to De data
...	currently not used.

Details

(Un-)logged model

When log = TRUE this function calculates the weighted mean of logarithmic De values. Each of the estimates is weighted by the inverse square of its relative standard error. The weighted mean is then transformed back to the dose scale (Galbraith & Roberts 2012, p. 14).

The log transformation is not applicable if the De estimates are close to zero or negative. In this case the un-logged model can be applied instead (`log = FALSE`). The weighted mean is then calculated using the un-logged estimates of De and their absolute standard error (Galbraith & Roberts 2012, p. 14).

Value

Returns a terminal output. In addition an `RLum.Results` object is returned containing the following element:

`summary`	data.frame summary of all relevant model results.
`data`	data.frame original input data
`args`	list used arguments
`call`	call the function call

The output should be accessed using the function `get_RLum.Results`

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team

References

Galbraith, R.F. & Laslett, G.M., 1993. Statistical models for mixed fission track ages. Nuclear Tracks Radiation Measurements 4, 459-470.

Galbraith, R.F., Roberts, R.G., Laslett, G.M., Yoshida, H. & Olley, J.M., 1999. Optical dating of single grains of quartz from Jinmium rock shelter, northern Australia. Part I: experimental design and statistical models. Archaeometry 41, 339-364.

Galbraith, R.F. & Roberts, R.G., 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: An overview and some recommendations. Quaternary Geochronology 11, 1-27.

Further reading

Arnold, L.J. & Roberts, R.G., 2009. Stochastic modelling of multi-grain equivalent dose (De) distributions: Implications for OSL dating of sediment mixtures. Quaternary Geochronology 4, 204-230.

Bailey, R.M. & Arnold, L.J., 2006. Statistical modelling of single grain quartz De distributions and an assessment of procedures for estimating burial dose. Quaternary Science Reviews 25, 2475-2502.

Cunningham, A.C. & Wallinga, J., 2012. Realizing the potential of fluvial archives using robust OSL chronologies. Quaternary Geochronology 12, 98-106.

Rodnight, H., Duller, G.A.T., Wintle, A.G. & Tooth, S., 2006. Assessing the reproducibility and accuracy of optical dating of fluvial deposits. Quaternary Geochronology 1, 109-120.

Rodnight, H., 2008. How many equivalent dose values are needed to obtain a reproducible distribution?. Ancient TL 26, 3-10.

See Also

calc_CentralDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MinDose

Examples

```
## load example data
data(ExampleData.DeValues, envir = environment())

## apply the common dose model
calc_CommonDose(ExampleData.DeValues$CA1)
```

---

calc_CosmicDoseRate *Calculate the cosmic dose rate*

Description

This function calculates the cosmic dose rate taking into account the soft- and hard-component of the cosmic ray flux and allows corrections for geomagnetic latitude, altitude above sea-level and geomagnetic field changes.

Usage

```
calc_CosmicDoseRate(depth, density, latitude, longitude, altitude,
    corr.fieldChanges = FALSE, est.age = NA, half.depth = FALSE,
    error = 10)
```

Arguments

depth	numeric (**required**): depth of overburden (m). For more than one absorber use c(depth_1, depth_2, ..., depth_n)
density	numeric (**required**): average overburden density (g/cm^3). For more than one absorber use c(density_1, density_2, ..., density_n)
latitude	numeric (**required**): latitude (decimal degree), N positive
longitude	numeric (**required**): longitude (decimal degree), E positive
altitude	numeric (**required**): altitude (m above sea-level)
corr.fieldChanges	logical (with default): correct for geomagnetic field changes after Prescott & Hutton (1994). Apply only when justified by the data.
est.age	numeric (with default): estimated age range (ka) for geomagnetic field change correction (0-80 ka allowed)
half.depth	logical (with default): How to overcome with varying overburden thickness. If TRUE only half the depth is used for calculation. Apply only when justified, i.e. when a constant sedimentation rate can safely be assumed.
error	numeric (with default): general error (percentage) to be implemented on corrected cosmic dose rate estimate

Details

This function calculates the total cosmic dose rate considering both the soft- and hard-component of the cosmic ray flux.

Internal calculation steps

(1) Calculate total depth of all absorber in hg/cm^2 (1 hg/cm^2 = 100 g/cm^2)

$$absorber = depth_1 * density_1 + depth_2 * density_2 + ... + depth_n * density_n$$

(2) If `half.depth = TRUE`

$$absorber = absorber/2$$

(3) Calculate cosmic dose rate at sea-level and 55 deg. latitude

a) If absorber is > 167 g/cm^2 (only hard-component; Allkofer et al. 1975): apply equation given by Prescott & Hutton (1994) (c.f. Barbouti & Rastin 1983)

$$D0 = C/(((absorber + d)^{\alpha} + a) * (absober + H)) * exp(-B * absorber)$$

b) If absorber is < 167 g/cm^2 (soft- and hard-component): derive D0 from Fig. 1 in Prescott & Hutton (1988).

(4) Calculate geomagnetic latitude (Prescott & Stephan 1982, Prescott & Hutton 1994)

$$\lambda = arcsin(0.203 * cos(latitude) * cos(longitude - 291) + 0.979 * sin(latitude))$$

(5) Apply correction for geomagnetic latitude and altitude above sea-level. Values for F, J and H were read from Fig. 3 shown in Prescott & Stephan (1982) and fitted with 3-degree polynomials for lambda < 35 degree and a linear fit for lambda > 35 degree.

$$Dc = D0 * (F + J * exp((altitude/1000)/H))$$

(6) Optional: Apply correction for geomagnetic field changes in the last 0-80 ka (Prescott & Hutton 1994). Correction and altitude factors are given in Table 1 and Fig. 1 in Prescott & Hutton (1994). Values for altitude factor were fitted with a 2-degree polynomial. The altitude factor is operated on the decimal part of the correction factor.

$$Dc' = Dc * correctionFactor$$

Usage of `depth` and `density`

(1) If only one value for depth and density is provided, the cosmic dose rate is calculated for exactly one sample and one absorber as overburden (i.e. `depth*density`).

(2) In some cases it might be useful to calculate the cosmic dose rate for a sample that is overlain by more than one absorber, e.g. in a profile with soil layers of different thickness and a distinct difference in density. This can be calculated by providing a matching number of values for `depth` and `density` (e.g. `depth = c(1, 2),density = c(1.7, 2.4)`)

(3) Another possibility is to calculate the cosmic dose rate for more than one sample of the same profile. This is done by providing more than one values for `depth` and only one for `density`. For example, `depth = c(1, 2, 3), density = 1.7` will calculate the cosmic dose rate for three samples in 1, 2 and 3 m depth in a sediment of density 1.7 g/cm^3.

Value

Returns a terminal output. In addition an RLum.Results object is returned containing the following element:

summary	data.frame summary of all relevant calculation results.
args	list used arguments
call	call the function call

The output should be accessed using the function get_RLum.Results

Function version

0.5.2 (2015-03-04 00:19:53)

Note

Despite its universal use the equation to calculate the cosmic dose rate provided by Prescott & Hutton (1994) is falsely stated to be valid from the surface to 10^4 hg/cm^2 of standard rock. The original expression by Barbouti & Rastin (1983) only considers the muon flux (i.e. hard-component) and is by their own definition only valid for depths between 10-10^4 hg/cm^2.

Thus, for near-surface samples (i.e. for depths < 167 g/cm^2) the equation of Prescott & Hutton (1994) underestimates the total cosmic dose rate, as it neglects the influence of the soft-component of the cosmic ray flux. For samples at zero depth and at sea-level the underestimation can be as large as ~0.1 Gy/ka. In a previous article, Prescott & Hutton (1988) give another approximation of Barbouti & Rastins equation in the form of

$$D = 0.21 * exp(-0.070 * absorber + 0.0005 * absorber^2)$$

which is valid for depths between 150-5000 g/cm^2. For shallower depths (< 150 g/cm^2) they provided a graph (Fig. 1) from which the dose rate can be read.

As a result, this function employs the equation of Prescott & Hutton (1994) only for depths > 167 g/cm^2, i.e. only for the hard-component of the cosmic ray flux. Cosmic dose rate values for depths < 167 g/cm^2 were obtained from the "AGE" programm (Gruen 2009) and fitted with a 6-degree polynomial curve (and hence reproduces the graph shown in Prescott & Hutton 1988). However, these values assume an average overburden density of 2 g/cm^3.

It is currently not possible to obtain more precise cosmic dose rate values for near-surface samples as there is no equation known to the author of this function at the time of writing.

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team

References

Allkofer, O.C., Carstensen, K., Dau, W.D., Jokisch, H., 1975. Letter to the editor. The absolute cosmic ray flux at sea level. Journal of Physics G: Nuclear and Particle Physics 1, L51-L52.

Barbouti, A.I., Rastin, B.C., 1983. A study of the absolute intensity of muons at sea level and under various thicknesses of absorber. Journal of Physics G: Nuclear and Particle Physics 9, 1577-1595.

Crookes, J.N., Rastin, B.C., 1972. An investigation of the absolute intensity of muons at sea-level. Nuclear Physics B 39, 493-508.

Gruen, R., 2009. The "AGE" program for the calculation of luminescence age estimates. Ancient TL 27, 45-46.

Prescott, J.R., Hutton, J.T., 1988. Cosmic ray and gamma ray dosimetry for TL and ESR. Nuclear Tracks and Radiation Measurements 14,

223-227. Prescott, J.R., Hutton, J.T., 1994. Cosmic ray contributions to dose rates for luminescence and ESR dating: large depths and long-term time variations. Radiation Measurements 23, 497-500.

Prescott, J.R., Stephan, L.G., 1982. The contribution of cosmic radiation to the environmental dose for thermoluminescence dating. Latitude, altitude and depth dependences. PACT 6, 17-25.

See Also

BaseDataSet.CosmicDoseRate

Examples

```
##(1) calculate cosmic dose rate (one absorber)
calc_CosmicDoseRate(depth = 2.78, density = 1.7,
                    latitude = 38.06451, longitude = 1.49646,
                    altitude = 364, error = 10)

##(2a) calculate cosmic dose rate (two absorber)
calc_CosmicDoseRate(depth = c(5.0, 2.78), density = c(2.65, 1.7),
                    latitude = 38.06451, longitude = 1.49646,
                    altitude = 364, error = 10)

##(2b) calculate cosmic dose rate (two absorber) and
##correct for geomagnetic field changes
calc_CosmicDoseRate(depth = c(5.0, 2.78), density = c(2.65, 1.7),
                    latitude = 12.04332, longitude = 4.43243,
                    altitude = 364, corr.fieldChanges = TRUE,
                    est.age = 67, error = 15)


##(3) calculate cosmic dose rate and export results to .csv file
#calculate cosmic dose rate and save to variable
results<- calc_CosmicDoseRate(depth = 2.78, density = 1.7,
                              latitude = 38.06451, longitude = 1.49646,
                              altitude = 364, error = 10)

# the results can be accessed by
get_RLum.Results(results, "summary")

#export results to .csv file - uncomment for usage
#write.csv(results, file = "c:/users/public/results.csv")

##(4) calculate cosmic dose rate for 6 samples from the same profile
##    and save to .csv file
#calculate cosmic dose rate and save to variable
```

```
results<- calc_CosmicDoseRate(depth = c(0.1, 0.5 , 2.1, 2.7, 4.2, 6.3),
                              density = 1.7, latitude = 38.06451,
                              longitude = 1.49646, altitude = 364,
                              error = 10)

#export results to .csv file - uncomment for usage
#write.csv(results, file = "c:/users/public/results_profile.csv")
```

`calc_FadingCorr` *Apply a fading correction according to Huntley & Lamothe (2001) for a given g-value.*

Description

This function runs the iterations that are needed to calculate the corrected age including the error for a given g-value according to Huntley & Lamothe (2001).

Usage

```
calc_FadingCorr(g_value, tc, age.faded, n.MCruns = 10000)
```

Arguments

`g_value`	vector (**required**): g-value and error obtained from separate fading measurements (see example)
`tc`	numeric (**required**): time in seconds (time between irradiation and the prompt measurement, cf. Huntely & Lamothe 2001)
`age.faded`	numeric vector (**required**): uncorrected age with error in ka (see example)
`n.MCruns`	integer (with default): number of Monte Carlo simulation runs for error estimation

Details

The error of the fading-corrected age is determined using a Monte Carlo simulation approach. Solving of the equation is realised using `uniroot` Large values for `n.MCruns` will significantly increase the computation time.

Value

Returns an S4 object of type `RLum.Results`. Slot `data` contains a `list` with the following structure:
$ age.corr (data.frame) .. $ age
.. $ age.error
$ age.corr.MC (numeric)

`Age.corr.MC` contain all possible ages from the Monte Carlo (error) simulation.

Function version

0.2 (2015-03-21 01:18:50)

Note

The upper age limit is set to 500 ka!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne R Luminescence Package Team

References

Huntley, D.J., Lamothe, M., 2001. Ubiquity of anomalous fading in K-feldspars and the measurement and correction for it in optical dating. Canadian Journal of Earth Sciences, 38, 1093-1106.

See Also

RLum.Results, get_RLum.Results, uniroot

Examples

```
results <- calc_FadingCorr(g_value = c(3.3,0.03), tc = 752,
                age.faded = c(100,10),
                n.MCruns=100)

get_RLum.Results(results)
```

---

calc_FiniteMixture *Apply the finite mixture model (FMM) after Galbraith (2005) to a given De distribution*

Description

This function fits a k-component mixture to a De distribution with differing known standard errors. Parameters (doses and mixing proportions) are estimated by maximum likelihood assuming that the log dose estimates are from a mixture of normal distributions.

Usage

```
calc_FiniteMixture(data, sigmab, n.components, grain.probability = FALSE,
    dose.scale, pdf.weight = TRUE, pdf.sigma = "sigmab", pdf.colors = "gray",
    pdf.scale, plot.proportions = TRUE, plot = TRUE, ...)
```

Arguments

data	RLum.Results or data.frame (**required**): for data.frame: two columns with De (data[,1]) and De error (values[,2])
sigmab	numeric (**required**): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Wallinga 2012, p. 100).

n.components	numeric (**required**): number of components to be fitted. If a vector is provided (e.g. c(2:8)) the finite mixtures for 2, 3 ... 8 components are calculated and a plot and a statistical evaluation of the model performance (BIC score and maximum log-likelihood) is provided.
grain.probability	logical (with default): prints the estimated probabilities of which component each grain is in
dose.scale	numeric: manually set the scaling of the y-axis of the first plot with a vector in the form of c(min,max)
pdf.weight	logical (with default): weight the probability density functions by the components proportion (applies only when a vector is provided for n.components)
pdf.sigma	character (with default): if "sigmab" the components normal distributions are plotted with a common standard deviation (i.e. sigmab) as assumed by the FFM. Alternatively, "se" takes the standard error of each component for the sigma parameter of the normal distribution
pdf.colors	character (with default): color coding of the components in the the plot. Possible options are "gray", "colors" and "none"
pdf.scale	numeric: manually set the max density value for proper scaling of the x-axis of the first plot
plot.proportions	logical (with default): plot barplot showing the proportions of components
plot	logical (with default): plot output
...	further arguments to pass. See details for their usage.

Details

This model uses the maximum likelihood and Bayesian Information Criterion (BIC) approaches.

Indications of overfitting are:

- increasing BIC
- repeated dose estimates
- covariance matrix not positive definite
- covariance matrix produces NaNs
- convergence problems

Plot

If a vector (c(k.min:k.max)) is provided for n.components a plot is generated showing the the k components equivalent doses as normal distributions. By default pdf.weight is set to FALSE, so that the area under each normal distribution is always 1. If TRUE, the probability density functions are weighted by the components proportion for each iteration of k components, so the sum of areas of each component equals 1. While the density values are on the same scale when no weights are used, the y-axis are individually scaled if the probability density are weighted by the components proportion.
The standard deviation (sigma) of the normal distributions is by default determined by a common sigmab (see pdf.sigma). For pdf.sigma = "se" the standard error of each component is taken instead.
The stacked barplot shows the proportion of each component (in per cent) calculated by the FFM. The last plot shows the achieved BIC scores and maximum log-likelihood estimates for each iteration of k.

Value

Returns a plot (optional) and terminal output. In addition an RLum.Results object is returned containing the following elements:

summary	data.frame summary of all relevant model results.
data	data.frame original input data
args	list used arguments
call	call the function call
mle	covariance matrices of the log likelihoods
BIC	BIC score
llik	maximum log likelihood
grain.probability	probabilities of a grain belonging to a component
components	matrix estimates of the de, de error and proportion for each component
single.comp	data.frame single componente FFM estimate

If a vector for n.components is provided (e.g. c(2:8)), mle and grain.probability are lists containing matrices of the results for each iteration of the model.

The output should be accessed using the function get_RLum.Results

Function version

0.4 (2015-03-04 13:33:56)

Author(s)

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2006.

R Luminescence Package Team

References

Galbraith, R.F. & Green, P.F., 1990. Estimating the component ages in a finite mixture. Nuclear Tracks and Radiation Measurements 17, 197-206.

Galbraith, R.F. & Laslett, G.M., 1993. Statistical models for mixed fission track ages. Nuclear Tracks Radiation Measurements 4, 459-470.

Galbraith, R.F. & Roberts, R.G., 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: An overview and some recommendations. Quaternary Geochronology 11, 1-27.

Roberts, R.G., Galbraith, R.F., Yoshida, H., Laslett, G.M. & Olley, J.M., 2000. Distinguishing dose populations in sediment mixtures: a test of single-grain optical dating procedures using mixtures of laboratory-dosed quartz. Radiation Measurements 32, 459-465.

Galbraith, R.F., 2005. Statistics for Fission Track Analysis, Chapman & Hall/CRC, Boca Raton.

Further reading

Arnold, L.J. & Roberts, R.G., 2009. Stochastic modelling of multi-grain equivalent dose (De) distributions: Implications for OSL dating of sediment mixtures. Quaternary Geochronology 4, 204-230.

Cunningham, A.C. & Wallinga, J., 2012. Realizing the potential of fluvial archives using robust OSL chronologies. Quaternary Geochronology 12, 98-106.

Rodnight, H., Duller, G.A.T., Wintle, A.G. & Tooth, S., 2006. Assessing the reproducibility and accuracy of optical dating of fluvial deposits. Quaternary Geochronology 1, 109-120.

Rodnight, H. 2008. How many equivalent dose values are needed to obtain a reproducible distribution?. Ancient TL 26, 3-10.

See Also

calc_CentralDose, calc_CommonDose, calc_FuchsLang2001, calc_MinDose

Examples

```
## load example data
data(ExampleData.DeValues, envir = environment())

## (1) apply the finite mixture model
## NOTE: the data set is not suitable for the finite mixture model,
## which is why a very small sigmab is necessary
calc_FiniteMixture(ExampleData.DeValues$CA1,
                   sigmab = 0.2, n.components = 2,
                   grain.probability = TRUE)

## (2) repeat the finite mixture model for 2, 3 and 4 maximum number of fitted
## components and save results
## NOTE: The following example is computationally intensive. Please un-comment
## the following lines to make the example work.
FMM<- calc_FiniteMixture(ExampleData.DeValues$CA1,
                         sigmab = 0.2, n.components = c(2:4),
                         pdf.weight = TRUE, dose.scale = c(0, 100))

## show structure of the results
FMM

## show the results on equivalent dose, standard error and proportion of
## fitted components
get_RLum.Results(object = FMM, data.object = "components")
```

---

calc_FuchsLang2001 *Apply the model after Fuchs & Lang (2001) to a given De distribution.*

Description

This function applies the method according to Fuchs & Lang (2001) for heterogeneously bleached samples with a given coefficient of variation threshold.

Usage

```
calc_FuchsLang2001(data, cvThreshold = 5, startDeValue = 1, plot = TRUE,
    ...)
```

Arguments

data	RLum.Results or data.frame (**required**): for data.frame: two columns with De (data[,1]) and De error (values[,2])
cvThreshold	numeric (with default): coefficient of variation in percent, as threshold for the method, e.g. cvThreshold = 3. See details.
startDeValue	numeric (with default): number of the first aliquot that is used for the calculations
plot	logical (with default): plot output TRUE/FALSE
...	further arguments and graphical parameters passed to plot

Details

Used values

If the coefficient of variation (c[v]) of the first two values is larger than the threshold c[v_threshold], the first value is skipped. Use the startDeValue argument to define a start value for calculation (e.g. 2nd or 3rd value).

Basic steps of the approach

(1) Estimate natural relative variation of the sample using a dose recovery test
(2) Sort the input values ascendingly
(3) Calculate a running mean, starting with the lowermost two values and add values iteratively.
(4) Stop if the calculated c[v] exceeds the specified cvThreshold

Value

Returns a plot (optional) and terminal output. In addition an RLum.Results object is returned containing the following elements:

summary	data.frame summary of all relevant model results.
data	data.frame original input data
args	list used arguments
call	call the function call
usedDeValues	data.frame containing the used values for the calculation

Function version

0.4.1 (2015-03-04 13:31:55)

Note

Please consider the requirements and the constraints of this method (see Fuchs & Lang, 2001)

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France) Christoph Burow, University of Cologne (Germany) R Luminescence Package Team

References

Fuchs, M. & Lang, A., 2001. OSL dating of coarse-grain fluvial quartz using single-aliqout protocols on sediments from NE Peloponnese, Greece. In: Quaternary Science Reviews 20, 783-787.

Fuchs, M. & Wagner, G.A., 2003. Recognition of insufficient bleaching by small aliquots of quartz for reconstructing soil erosion in Greece. Quaternary Science Reviews 22, 1161-1167.

See Also

plot, calc_MinDose, calc_FiniteMixture, calc_CentralDose, calc_CommonDose, RLum.Results

Examples

```
##load example data
data(ExampleData.DeValues, envir = environment())

##calculate De according to Fuchs & Lang (2001)
temp<- calc_FuchsLang2001(ExampleData.DeValues$BT998, cvThreshold = 5)
```

---

calc_HomogeneityTest *Apply a simple homogeneity test after Galbraith (2003)*

Description

A simple homogeneity test for De estimates

Usage

```
calc_HomogeneityTest(data, log = TRUE, ...)
```

Arguments

data	RLum.Results or data.frame (**required**): for data.frame: two columns with De (data[,1]) and De error (values[,2])
log	logical (with default): peform the homogeniety test with (un-)logged data
...	further arguments (for internal compatibility only).

Details

For details see Galbraith (2003).

Value

Returns a terminal output. In addition an RLum.Results object is returned containing the following element:

summary	data.frame summary of all relevant model results.
data	data.frame original input data
args	list used arguments
call	call the function call

The output should be accessed using the function get_RLum.Results

Function version

0.2 (2015-03-04 13:31:44)

Author(s)

Christoph Burow, University of Cologne (Germany),
R Luminescence Package Team

References

Galbraith, R.F., 2003. A simple homogeneity test for estimates of dose obtained using OSL. Ancient TL 21, 75-77.

See Also

pchisq

Examples

```
## load example data
data(ExampleData.DeValues, envir = environment())

## apply the homogeneity test
calc_HomogeneityTest(ExampleData.DeValues$BT998)
```

---

calc_IEU *Apply the internal-external-uncertainty (IEU) model after Thomsen et al. (2007) to a given De distribution*

Description

Function to calculate the IEU De for a De data set.

Usage

```
calc_IEU(data, a, b, interval, decimal.point = 2, plot = TRUE,
    ...)
```

Arguments

data	RLum.Results or data.frame (**required**): for data.frame: two columns with De (data[,1]) and De error (values[,2])
a	numeric: slope
b	numeric: intercept
interval	numeric: fixed interval (e.g. 5 Gy) used for iteration of Dbar, from the mean to Lowest.De used to create Graph.IEU [Dbar.Fixed vs Z]
decimal.point	numeric (with default): number of decimal points for rounding calculations (e.g. 2)
plot	logical (with default): plot output
...	further arguments (trace, verbose).

Details

This function uses the equations of Thomsen et al. (2007). The parameters a and b are estimated from dose-recovery experiments.

Value

Returns a plot (optional) and terminal output. In addition an RLum.Results object is returned containing the following element:

summary	data.frame summary of all relevant model results.
data	data.frame original input data
args	list used arguments
call	call the function call
tables	list a list of data frames containing all calculation tables

The output should be accessed using the function get_RLum.Results.

Function version

0.1 (2015-03-04 13:18:38)

Author(s)

Rachel Smedley, Geography & Earth Sciences, Aberystwyth University (United Kingdom)
Based on an excel spreadsheet and accompanying macro written by Kristina Thomsen. R Luminescence Package Team

References

Thomsen, K.J., Murray, A.S., Boetter-Jensen, L. & Kinahan, J., 2007. Determination of burial dose in incompletely bleached fluvial samples using single grains of quartz. Radiation Measurements 42, 370-379.

See Also

plot, calc_CommonDose, calc_CentralDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MinDose

Examples

```
## load data
data(ExampleData.DeValues, envir = environment())

## apply the IEU model
ieu <- calc_IEU(ExampleData.DeValues$CA1, a = 0.2, b = 1.9, interval = 1)
```

`calc_MaxDose` *Apply the maximum age model to a given De distribution*

Description

Function to fit the maximum age model to De data. This is a wrapper function that calls calc_MinDose() and applies a similiar approach as described in Olley et al. (2006).

Usage

```
calc_MaxDose(data, sigmab, log = TRUE, par = 3, bootstrap = FALSE,
    init.values, plot = TRUE, ...)
```

Arguments

`data`	`RLum.Results` or data.frame (**required**): for `data.frame`: two columns with De (`data[,1]`) and De error (`values[,2]`)
`sigmab`	`numeric` (**required**): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
`log`	`logical` (with default): fit the (un-)logged three parameter minimum dose model to De data
`par`	`numeric` (with default): apply the 3- or 4-parametric minimum age model (`par=3` or `par=4`).
`bootstrap`	
`init.values`	`numeric` (with default): starting values for gamma, sigma, p0 and mu. Custom values need to be provided in a vector of length three in the form of `c(gamma, sigma, p0)`.
`plot`	`logical` (with default): plot output (`TRUE`/`FALSE`)
`...`	further arguments for bootstrapping (`bs.M, bs.N, bs.h, sigmab.sd`). See details for their usage.

Details

Data transformation

To estimate the maximum dose population and its standard error, the three parameter minimum age model of Galbraith et al. (1999) is adapted. The measured De values are transformed as follows:

1. convert De values to natural logs

2. multiply the logged data to creat a mirror image of the De distribution
3. shift De values along x-axis by the smallest x-value found to obtain only positive values
4. combine in quadrature the measurement error associated with each De value with a relative error specified by sigmab
5. apply the MAM to these data

When all calculations are done the results are then converted as follows

1. subtract the x-offset
2. multiply the natural logs by -1
3. take the exponent to obtain the maximum dose estimate in Gy

Further documentation

Please see `calc_MinDose`.

Value

Please see `calc_MinDose`.

Function version

0.3 (2015-03-04 13:31:23)

Author(s)

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2010

R Luminescence Package Team

References

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Further reading

Arnold, L.J. & Roberts, R.G., 2009. Stochastic modelling of multi-grain equivalent dose (De) distributions: Implications for OSL dating of sediment mixtures. Quaternary Geochronology 4, 204-230.

Bailey, R.M. & Arnold, L.J., 2006. Statistical modelling of single grain quartz De distributions and an assessment of procedures for estimating burial dose. Quaternary Science Reviews 25, 2475-2502.

Cunningham, A.C. & Wallinga, J., 2012. Realizing the potential of fluvial archives using robust OSL chronologies. Quaternary Geochronology 12, 98-106.

Rodnight, H., Duller, G.A.T., Wintle, A.G. & Tooth, S., 2006. Assessing the reproducibility and accuracy of optical dating of fluvial deposits. Quaternary Geochronology 1, 109-120.

Rodnight, H., 2008. How many equivalent dose values are needed to obtain a reproducible distribution?. Ancient TL 26, 3-10.

See Also

calc_CentralDose, calc_CommonDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MinDose

Examples

```
## load example data
data(ExampleData.DeValues, envir = environment())

# apply the maximum dose model
calc_MaxDose(ExampleData.DeValues$CA1, sigmab = 0.2, par = 3)
```

---

calc_MinDose *Apply the (un-)logged minimum age model (MAM) after Galbraith et al. (1999) to a given De distribution*

Description

Function to fit the (un-)logged three or four parameter minimum dose model (MAM-3/4) to De data.

Usage

```
calc_MinDose(data, sigmab, log = TRUE, par = 3, bootstrap = FALSE,
    init.values, plot = TRUE, multicore = FALSE, ...)
```

Arguments

data	RLum.Results or data.frame (**required**): for data.frame: two columns with De (data[,1]) and De error (values[,2])

sigmab	numeric (**required**): spread in De values given as a fraction (e.g. 0.2). This value represents the expected overdispersion in the data should the sample be well-bleached (Cunningham & Walling 2012, p. 100).
log	logical (with default): fit the (un-)logged minimum dose model to De data
par	numeric (with default): apply the 3- or 4-parametric minimum age model (par=3 or par=4). The MAM-3 is used by default.
bootstrap	logical (with default): apply the recycled bootstrap approach of Cunningham & Wallinga (2012).
init.values	numeric (optional): a named list with starting values for gamma, sigma, p0 and mu (e.g. list(gamma=100 sigma=1.5, p0=0.1, mu=100)). If no values are provided reasonable values are tried to be estimated from the data.
plot	logical (with default): plot output (TRUE/FALSE)
multicore	logical (with default): enable parallel computation of the bootstrap by creating a multicore SNOW cluster. Depending on the number of available logical CPU cores this will drastically reduce the computation time. Note that this option is highly experimental and not work for all machines. (TRUE/FALSE)
...	(optional) further arguments for bootstrapping (bs.M, bs.N, bs.h, sigmab.sd). See details for their usage. Further arguments are verbose to de-/activate console output (logical), debug for extended console output (logical) and cores (integer) to manually specify the number of cores to be used when multicore=TRUE.

Details

Parameters

This model has four parameters:

gamma:	minimum dose on the log scale
mu:	mean of the non-truncated normal distribution
sigma:	spread in ages above the minimum
p0:	proportion of grains at gamma

If par=3 (default) the 3-parametric minimum age model is applied, where gamma=mu. For par=4 the 4-parametric model is applied instead.

(Un-)logged model

In the original version of the three-parameter minimum dose model, the basic data are the natural logarithms of the De estimates and relative standard errors of the De estimates. This model will be applied if log=TRUE.

If log=FALSE, the modified un-logged model will be applied instead. This has essentially the same form as the original version. gamma and sigma are in Gy and gamma becomes the minimum true dose in the population.

While the original (logged) version of the mimimum dose model may be appropriate for most samples (i.e. De distributions), the modified (un-logged) version is specially designed for modern-age

and young samples containing negative, zero or near-zero De estimates (Arnold et al. 2009, p. 323).

Initial values & boundaries

The log likelihood calculations use the nlminb function for box-constrained optimisation using PORT routines. Accordingly, initial values for the four parameters can be specified via `init.values`. If no values are provided for `init.values` reasonable starting values are estimated from the input data. If the final estimates of *gamma*, *mu*, *sigma* and *p0* are totally off target, consider providing custom starting values via `init.values`.
In contrast to previous versions of this function the boundaries for the individual model parameters can no longer be specified. Appropriate boundary are now hard-coded and are valid for all input data sets.

Bootstrap

When `bootstrap=TRUE` the function applies the bootstrapping method as described in Wallinga & Cunningham (2012). By default, the minimum age model produces 1000 first level and 3000 second level bootstrap replicates (actually, the number of second level bootstrap replicates is three times the number of first level replicates unless specified otherwise). The uncertainty on sigmab is 0.04 by default. These values can be changed by using the arguments `bs.M` (first level replicates), `bs.N` (second level replicates) and `sigmab.sd` (error on sigmab). With `bs.h` the bandwidth of the kernel density estimate can be specified. By default, `h` is calculated as

$$h = (2 * \sigma_{DE})/\sqrt{n}$$

Multicore support

This function supports parallel computing and can be activated by `multicore=TRUE`. By default, the number of available logical CPU cores is determined automatically, but can be changed with `cores`. The multicore support is only available when `bootstrap=TRUE` and spawns `n` R instances for each core to get MAM estimates for each of the N and M boostrap replicates. Note that this option is highly experimental and may or may not work for your machine. Also the performance gain increases for larger number of bootstrap replicates. Also note that with each additional core and hence R instance and depending on the number of bootstrap replicates the memory usage can significantly increase. Make sure that memory is always availabe, otherwise there will be a massive perfomance hit.

Value

Returns a plot (optional) and terminal output. In addition an `RLum.Results` object is returned containing the following elements:

`summary`	data.frame summary of all relevant model results.
`data`	data.frame original input data
`args`	list used arguments
`call`	call the function call
`mle`	mle2 object containing the maximum log likelihood functions for all parameters
`BIC`	numeric BIC score
`confint`	data.frame confidence intervals for all parameters
`profile`	profile.mle2 the log likelihood profiles

`bootstrap` list bootstrap results

The output should be accessed using the function `get_RLum.Results`

Function version

0.4.1 (2015-03-18 13:29:54)

Note

The default starting values for *gamma*, *mu*, *sigma* and *p0* may only be appropriate for some De data sets and may need to be changed for other data. This is especially true when the un-logged version is applied.
Also note that all R warning messages are suppressed when running this function. If the results seem odd consider re-running the model with `debug=TRUE` which provides extended console output and forwards all internal warning messages.

Author(s)

Christoph Burow, University of Cologne (Germany)
Based on a rewritten S script of Rex Galbraith, 2010
The bootstrap approach is based on a rewritten MATLAB script of Alastair Cunningham.
Alastair Cunningham is thanked for his help in implementing and cross-checking the code.
R Luminescence Package Team

References

Arnold, L.J., Roberts, R.G., Galbraith, R.F. & DeLong, S.B., 2009. A revised burial dose estimation procedure for optical dating of young and modern-age sediments. Quaternary Geochronology 4, 306-325.

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Galbraith, R.F., 2005. Statistics for Fission Track Analysis, Chapman & Hall/CRC, Boca Raton.

Galbraith, R.F. & Roberts, R.G., 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: An overview and some recommendations. Quaternary Geochronology 11, 1-27.

Further reading

Arnold, L.J. & Roberts, R.G., 2009. Stochastic modelling of multi-grain equivalent dose (De) distributions: Implications for OSL dating of sediment mixtures. Quaternary Geochronology 4, 204-230.

Bailey, R.M. & Arnold, L.J., 2006. Statistical modelling of single grain quartz De distributions and an assessment of procedures for estimating burial dose. Quaternary Science Reviews 25, 2475-2502.

Cunningham, A.C. & Wallinga, J., 2012. Realizing the potential of fluvial archives using robust

OSL chronologies. Quaternary Geochronology 12, 98-106.

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Rodnight, H., 2008. How many equivalent dose values are needed to obtain a reproducible distribution?. Ancient TL 26, 3-10.

See Also

calc_CentralDose, calc_CommonDose, calc_FiniteMixture, calc_FuchsLang2001, calc_MaxDose

Examples

```
## Load example data
data(ExampleData.DeValues, envir = environment())

# (1) Apply the minimum age model with minimum required parameters.
# By default, this will apply the un-logged 3-parametric MAM.
calc_MinDose(data = ExampleData.DeValues$CA1, sigmab = 0.1)

# (2) Re-run the model, but save results to a variable and turn
# plotting of the log-likelihood profiles off.
mam <- calc_MinDose(data = ExampleData.DeValues$CA1,
                    sigmab = 0.1,
                    plot = FALSE)

# Show structure of the RLum.Results object
mam

# Show summary table that contains the most relevant results
res <- get_RLum.Results(mam, "summary")
res

# Plot the log likelihood profiles retroactively, because before
# we set plot = FALSE
plot_RLum.Results(mam)

# Plot the dose distribution in an abanico plot and draw a line
# at the minimum dose estimate
plot_AbanicoPlot(data = ExampleData.DeValues$CA1,
                 main = "3-parameter Minimum Age Model",
                 line = mam,polygon.col = "none",
                 hist = TRUE,
                 rug = TRUE,
                 summary = c("n", "mean", "mean.weighted", "median", "in.ci"),
                 centrality = res$de,
                 line.col = "red",
                 grid.col = "none",
                 line.label = paste0(round(res$de, 1), "\U00B1",
                                     round(res$de_err, 1), " Gy"),
                 bw = 0.1,
                 ylim = c(-25, 18),
```

```
                  summary.pos = "topleft",
                  mtext = bquote("Parameters: " ~
                                 sigma[b] == .(get_RLum(mam, "args")$sigmab) ~ ", " ~
                                 gamma == .(round(log(res$de), 1)) ~ ", " ~
                                 sigma == .(round(res$sig, 1)) ~ ", " ~
                                 rho == .(round(res$p0, 2))))

# (3) Run the minimum age model with bootstrap
# NOTE: Bootstrapping is computationally intensive, which is why the
# following example is commented out. To run the examples just
# uncomment the code.
# (3.1) run the minimum age model with default values for bootstrapping
#calc_MinDose(data = ExampleData.DeValues$CA1,
#             sigmab = 0.15,
#             bootstrap = TRUE)

# (3.2) Bootstrap control parameters
#mam <- calc_MinDose(data = ExampleData.DeValues$CA1,
#                    sigmab = 0.15,
#                    bootstrap = TRUE,
#                    bs.M = 300,
#                    bs.N = 500,
#                    bs.h = 4,
#                    sigmab.sd = 0.06,
#                    plot = FALSE)

# Plot the results
#plot_RLum(mam)

# save bootstrap results in a separate variable
#bs <- get_RLum.Results(mam, "bootstrap")

# show structure of the bootstrap results
#str(bs, max.level = 2, give.attr = FALSE)

# print summary of minimum dose and likelihood pairs
#summary(bs$pairs$gamma)

# Show polynomial fits of the bootstrap pairs
#bs$poly.fits$poly.three

# Plot various statistics of the fit using the generic plot() function
#par(mfcol=c(2,2))
#plot(bs$poly.fits$poly.three, ask = FALSE)

# Show the fitted values of the polynomials
#summary(bs$poly.fits$poly.three$fitted.values)
```

`calc_OSLLxTxRatio` *Calculate Lx/Tx ratio for CW-OSL curves*

Description

Calculate Lx/Tx ratios from a given set of CW-OSL curves.

Usage

```
calc_OSLLxTxRatio(Lx.data, Tx.data, signal.integral, background.integral,
    background.count.distribution = "non-poisson", sigmab)
```

Arguments

`Lx.data`	data.frame (**required**): requires a CW-OSL shine down curve (x = time, y = counts)
`Tx.data`	data.frame (optional): requires a CW-OSL shine down curve (x = time, y = counts). If no input is given the Tx.data will be treated as `NA` and no Lx/Tx ratio is calculated.
`signal.integral`	vector (**required**): vector with the limits for the signal integral.
`background.integral`	vector (**required**): vector with the bounds for the background integral.
`background.count.distribution`	character (with default): Sets the count distribution assumed for the error calculation. Possible arguments `poisson` or `non-poisson`. See details for further information
`sigmab`	numeric (optional): Option to set a manual value for the overdispersion (for LnTx and TnTx), used for the Lx/Tx error calculation. The value should be provided as absolute squared count values, e.g. `sigmab = c(300,300)`. Note: If only one value is provided this value is taken for both (LnTx and TnTx) signals.

Details

The integrity of the chosen values for the signal and background integral is checked by the function; the signal integral limits have to be lower than the background integral limits. If a vector is given as input instead of a data.frame, an artificial `data.frame` is produced. The error calculation is done according to Galbraith (2002).

background.count.distribution

This argument allows selecting the distribution assumption that is used for the error calculation. According to Galbraith (2002, 2014) the background counts may be overdispersed (i.e. do not follow a poisson distribution, which is assumed for the photomultiplier counts). In that case (might be the normal case) it has to be accounted for the overdispersion by estimating σ^2 (i.e. the overdispersion value). Therefore the relative standard error is calculated as:

(a) `poisson`

$$rse(\mu_S) \approx \sqrt{(Y_0 + Y_1/k^2)/Y_0 - Y_1/k}$$

(b) `non-poisson`

$$rse(\mu_S) \approx \sqrt{(Y_0 + Y_1/k^2 + \sigma^2(1 + 1/k))/Y_0 - Y_1/k}$$

Value

Returns an S4 object of type `RLum.Results`. Slot `data` contains a `list` with the following structure: $ LxTx.table (data.frame) .. $ LnLx

.. $ LnLx.BG
.. $ TnTx
.. $ TnTx.BG
.. $ Net_LnLx
.. $ Net_LnLx.Error
.. $ Net_TnTx.Error
.. $ LxTx
.. $ LxTx.Error
$ calc.parameters (list)
.. $ sigmab.LnTx
.. $ sigmab.TnTx
.. $ k

Function version

0.4.5 (2015-03-04 00:19:53)

Note

The results of this function have been cross-checked with the Analyst (vers. 3.24b). Access to the results object via `get_RLum.Results`.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
R Luminescence Package Team

References

Duller, G., 2007. Analyst. http://www.nutech.dtu.dk/english/~/media/Andre_Universitetsenheder/Nutech/Produkter%20og%20services/Dosimetri/radiation_measurement_instruments/tl_osl_reader/Manuals/analyst_manual_v3_22b.ashx

Galbraith, R.F., 2002. A note on the variance of a background-corrected OSL count. Ancient TL, 20 (2), 49-51.

Galbraith, R.F., 2014. A further note on the variance of a background-corrected OSL count. Ancient TL, 31 (2), 1-3.

See Also

`Analyse_SAR.OSLdata`, `plot_GrowthCurve`, `analyse_SAR.CWOSL`

Examples

```
##load data
data(ExampleData.LxTxOSLData, envir = environment())

##calculate Lx/Tx ratio
results <- calc_OSLLxTxRatio(Lx.data, Tx.data, signal.integral = c(1:2),
                             background.integral = c(85:100))

##get results object
get_RLum.Results(results)
```

`calc_SourceDoseRate` *Calculation of the source dose rate via the date of measurement*

Description

Calculating the dose rate of the irradiation source via the date of measurement based on: source calibration date, source dose rate, dose rate error. The function returns a data.frame that provides the input argument dose_rate for the function `Second2Gray`.

Usage

```
calc_SourceDoseRate(measurement.date, calib.date, calib.dose.rate,
    calib.error, source.type = "Sr-90", dose.rate.unit = "Gy/s")
```

Arguments

`measurement.date`	`character` (**required**): date of measurement in "YYYY-MM-DD"
`calib.date`	`character` (**required**): date of source calibration in "YYYY-MM-DD"
`calib.dose.rate`	`numeric` (**required**): dose rate at date of calibration in Gy/s or Gy/min
`calib.error`	`numeric` (**required**): error of dose rate at date of calibration Gy/s or Gy/min
`source.type`	`character` (with default): specify irrdiation source (`Sr-90` or `Co-60` or `Am-214`), see details for further information
`dose.rate.unit`	`character` (with default): specify dose rate unit for input (`Gy/min` or `Gy/s`), the output is given in Gy/s as valid for the function `Second2Gray`

Details

Calculation of the source dose rate based on the time elapsed since the last calibration of the irradiation source. Decay parameters assume a Sr-90 beta source.

$$dose.rate = D0 * exp(-log(2)/T.1/2 * t)$$

with: D0 <- calibration dose rate T.1/2 <- half-life of the source nuclide (here in days) t <- time since source calibration (in days) log(2) / T.1/2 equals the decay constant lambda

Information on the date of measurements may be taken from the data's original .BIN file (using e.g., BINfile <- readBIN2R() and the slot BINfile@METADATA$DATE)

Allowed source types and related values

#	Source type	T.1/2	Reference
[1]	Sr-90	28.90 y	NNDC, Brookhaven National Laboratory
[2]	Am-214	432.6 y	NNDC, Brookhaven National Laboratory
[3]	Co-60	5.274 y	NNDC, Brookhaven National Laboratory

Value

Returns an S4 object of type RLum.Results. Slot data contains a list with the following structure:
$ dose.rate (data.frame)
.. $ dose.rate
.. $ dose.rate.error
$ parameters (list)
.. $ source.type
.. $ halflife
.. $ dose.rate.unit

Function version

0.1 (2015-03-04 14:33:28)

Note

#

Author(s)

Margret C. Fuchs, AWI Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

NNDC, Brookhaven National Laboratory (http://www.nndc.bnl.gov/)

See Also

Second2Gray

Examples

```
##(1) Simple function usage
##Basic calculation of the dose rate for a specific date
dose.rate <-  calc_SourceDoseRate(measurement.date = "2012-01-27",
                                  calib.date = "2014-12-19",
                                  calib.dose.rate = 0.0438,
                                  calib.error = 0.0019)

##show results
get_RLum.Results(dose.rate)

##(2) Usage in combination with another function (e.g., Second2Gray() )
## load example data
data(ExampleData.DeValues, envir = environment())

## use the calculated variable dose.rate as input argument
## to convert De(s) to De(Gy)
Second2Gray(ExampleData.DeValues$BT998, dose.rate)
```

calc_Statistics *Function to calculate statistic measures*

Description

This function calculates a number of descriptive statistics for De-data, most fundamentally using error-weighted approaches.

Usage

```
calc_Statistics(data, weight.calc = "reciprocal", na.rm = TRUE)
```

Arguments

data	data.frame or RLum.Results object (required): for data.frame two columns: De (data[,1]) and De error (data[,2]). To plot several data sets in one plot the data sets must be provided as list, e.g. list(data.1, data.2).
weight.calc	character: type of weight calculation. One out of "reciprocal" (weight is 1/error), "square" (weight is 1/error^2).
na.rm	logical (with default): indicating whether NA values should be stripped before the computation proceeds.

Value

Returns a list with weighted and unweighted statistic measures.

Function version

0.1.1 (2015-03-04 17:27:01)

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
R Luminescence Package Team

Examples

```
## load example data
data(ExampleData.DeValues, envir = environment())

## show a rough plot of the data to illustrate the non-normal distribution
plot_KDE(ExampleData.DeValues$BT998)

## calculate statistics and show output
str(calc_Statistics(ExampleData.DeValues$BT998))

## now the same for 10000 normal distributed random numbers with equal errors
x <- as.data.frame(cbind(rnorm(n = 10^5, mean = 0, sd = 1),
                         rep(0.001, 10^5)))

## note the congruent results for weighted and unweighted measures
str(calc_Statistics(x))
```

`calc_TLLxTxRatio` *Calculate the Lx/Tx ratio for a given set of TL curves [beta version]*

Description

Calculate Lx/Tx ratio for a given set of TL curves.

Usage

```
calc_TLLxTxRatio(Lx.data.signal, Lx.data.background, Tx.data.signal,
    Tx.data.background, signal.integral.min, signal.integral.max)
```

Arguments

`Lx.data.signal`	data.frame (**required**): TL data (x = temperature, y = counts) (TL signal)
`Lx.data.background`	data.frame (optional): TL data (x = temperature, y = counts). If no data are provided no background subtraction is performed.
`Tx.data.signal`	data.frame (**required**): TL data (x = temperature, y = counts) (TL test signal)
`Tx.data.background`	data.frame (optional): TL data (x = temperature, y = counts). If no data are provided no background subtraction is performed.
`signal.integral.min`	integer (**required**): channel number for the lower signal integral bound (e.g. `signal.integral.min = 100`)
`signal.integral.max`	integer (**required**): channel number for the upper signal integral bound (e.g. `signal.integral.max = 200`)

Details

-

Value

Returns an S4 object of type `RLum.Results`. Slot `data` contains a list with the following structure:

$ LxTx.table
.. $ LnLx
.. $ LnLx.BG
.. $ TnTx
.. $ TnTx.BG
.. $ Net_LnLx
.. $ Net_LnLx.Error

Function version

0.3 (2015-03-04 00:19:53)

Note

This function has still BETA status!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Christoph Schmidt, University of Bayreuth (Germany),
R Luminescence Package Team

References

-

See Also

RLum.Results, analyse_SAR.TL

Examples

```
##load package example data
data(ExampleData.BINfileData, envir = environment())

##convert Risoe.BINfileData into a curve object
temp <- Risoe.BINfileData2RLum.Analysis(TL.SAR.Data, pos = 3)


Lx.data.signal <- get_RLum.Analysis(temp, record.id=1)
Lx.data.background <- get_RLum.Analysis(temp, record.id=2)
Tx.data.signal <- get_RLum.Analysis(temp, record.id=3)
Tx.data.background <- get_RLum.Analysis(temp, record.id=4)
signal.integral.min <- 210
signal.integral.max <- 230

output <- calc_TLLxTxRatio(Lx.data.signal,
                           Lx.data.background,
                           Tx.data.signal, Tx.data.background,
                           signal.integral.min, signal.integral.max)
get_RLum.Results(output)
```

CW2pHMi *Transform a CW-OSL curve into a pHM-OSL curve via interpolation under hyperbolic modulation conditions*

Description

This function transforms a conventionally measured continuous-wave (CW) OSL-curve to a pseudo hyperbolic modulated (pHM) curve under hyperbolic modulation conditions using the interpolation procedure described by Bos & Wallinga (2012).

Usage

```
CW2pHMi(values, delta)
```

Arguments

values	RLum.Data.Curve or data.frame (**required**): RLum.Data.Curve or data.frame with measured curve data of type stimulation time (t) (values[,1]) and measured counts (cts) (values[,2]).
delta	vector (optional): stimulation rate parameter, if no value is given, the optimal value is estimated automatically (see details). Smaller values of delta produce more points in the rising tail of the curve.

Details

The complete procedure of the transformation is described in Bos & Wallinga (2012). The input data.frame consists of two columns: time (t) and count values (CW(t))

Internal transformation steps

(1) log(CW-OSL) values

(2) Calculate t' which is the transformed time:

$$t' = t - (1/\delta) * log(1 + \delta * t)$$

(3) Interpolate CW(t'), i.e. use the log(CW(t)) to obtain the count values for the transformed time (t'). Values beyond min(t) and max(t) produce NA values.

(4) Select all values for t' < min(t), i.e. values beyond the time resolution of t. Select the first two values of the transformed data set which contain no NA values and use these values for a linear fit using lm.

(5) Extrapolate values for t' < min(t) based on the previously obtained fit parameters.

(6) Transform values using

$$pHM(t) = (\delta * t/(1 + \delta * t)) * c * CW(t')$$

$$c = (1 + \delta * P)/\delta * P$$

$$P = length(stimulation\ period)$$

(7) Combine all values and truncate all values for t' > max(t)

The number of values for t' < min(t) depends on the stimulation rate parameter delta*. To avoid the production of too many artificial data at the raising tail of the determined pHM curve, it is recommended to use the automatic estimation routine for* delta*, i.e. provide no value for* delta*.*

Value

The function returns the same data type as the input data type with the transformed curve values.

RLum.Data.Curve

package RLum object with two additional info elements:

$CW2pHMi.x.t	: transformed time values
$CW2pHMi.method	: used method for the production of the new data points

data.frame with four columns:

$x	: time
$y.t	: transformed count values
$x.t	: transformed time values
$method	: used method for the production of the new data points

Function version

0.2.2 (2015-03-04 18:42:57)

Note

According to Bos & Wallinga (2012), the number of extrapolated points should be limited to avoid artificial intensity data. If `delta` is provided manually and more than two points are extrapolated, a warning message is returned.

The function `approx` may produce some `Inf` and `NaN` data. The function tries to manually interpolate these values by calculating the `mean` using the adjacent channels. If two invalid values are succeeding, the values are removed and no further interpolation is attempted.
In every case a warning message is shown.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

Based on comments and suggestions from:
Adrie J.J. Bos, Delft University of Technology, The Netherlands

R Luminescence Package Team

References

Bos, A.J.J. & Wallinga, J., 2012. How to visualize quartz OSL signal components. Radiation Measurements, 47, 752-758.

Further Reading

Bulur, E., 1996. An Alternative Technique For Optically Stimulated Luminescence (OSL) Experiment. Radiation Measurements, 26, 701-709.

Bulur, E., 2000. A simple transformation for converting CW-OSL curves to LM-OSL curves. Radiation Measurements, 32, 141-145.

See Also

`CW2pLM`, `CW2pLMi`, `CW2pPMi`, `fit_LMCurve`, `lm`, `RLum.Data.Curve`

Examples

```
##(1) - simple transformation

##load CW-OSL curve data
data(ExampleData.CW_OSL_Curve, envir = environment())
```

```
##transform values
values.transformed<-CW2pHMi(ExampleData.CW_OSL_Curve)

##plot
plot(values.transformed$x, values.transformed$y.t, log = "x")

##(2) - load CW-OSL curve from BIN-file and plot transformed values

##load BINfile
#BINfileData<-readBIN2R("[path to BIN-file]")
data(ExampleData.BINfileData, envir = environment())

##grep first CW-OSL curve from ALQ 1

curve.ID<-CWOSL.SAR.Data@METADATA[CWOSL.SAR.Data@METADATA[,"LTYPE"]=="OSL" &
                                    CWOSL.SAR.Data@METADATA[,"POSITION"]==1
                                  ,"ID"]

curve.HIGH<-CWOSL.SAR.Data@METADATA[CWOSL.SAR.Data@METADATA[,"ID"]==curve.ID[1]
                                    ,"HIGH"]

curve.NPOINTS<-CWOSL.SAR.Data@METADATA[CWOSL.SAR.Data@METADATA[,"ID"]==curve.ID[1]
                                       ,"NPOINTS"]

##combine curve to data set

curve<-data.frame(x = seq(curve.HIGH/curve.NPOINTS,curve.HIGH,
                          by = curve.HIGH/curve.NPOINTS),
                  y=unlist(CWOSL.SAR.Data@DATA[curve.ID[1]]))


##transform values

curve.transformed <- CW2pHMi(curve)

##plot curve
plot(curve.transformed$x, curve.transformed$y.t, log = "x")


##(3) - produce Fig. 4 from Bos & Wallinga (2012)

##load data
data(ExampleData.CW_OSL_Curve, envir = environment())
values <- CW_Curve.BosWallinga2012

##open plot area
plot(NA, NA,
     xlim=c(0.001,10),
     ylim=c(0,8000),
     ylab="pseudo OSL (cts/0.01 s)",
     xlab="t [s]",
     log="x",
     main="Fig. 4 - Bos & Wallinga (2012)")

values.t<-CW2pLMi(values, P=1/20)
lines(values[1:length(values.t[,1]),1],CW2pLMi(values, P=1/20)[,2],
```

```
      col="red" ,lwd=1.3)
text(0.03,4500,"LM", col="red" ,cex=.8)

values.t<-CW2pHMi(values, delta=40)
lines(values[1:length(values.t[,1]),1],CW2pHMi(values, delta=40)[,2],
      col="black", lwd=1.3)
text(0.005,3000,"HM", cex=.8)

values.t<-CW2pPMi(values, P=1/10)
lines(values[1:length(values.t[,1]),1],CW2pPMi(values, P=1/10)[,2],
      col="blue", lwd=1.3)
text(0.5,6500,"PM", col="blue" ,cex=.8)
```

`CW2pLM` *Transform a CW-OSL curve into a pLM-OSL curve*

Description

Transforms a conventionally measured continuous-wave (CW) curve into a pseudo linearly modulated (pLM) curve using the equations given in Bulur (2000).

Usage

```
CW2pLM(values)
```

Arguments

`values`	`RLum.Data.Curve` or `data.frame` (**required**): `RLum.Data.Curve` data object. Alternatively, a `data.frame` of the measured curve data of type stimulation time (t) (`values[,1]`) and measured counts (cts) (`values[,2]`) can be provided.

Details

According to Bulur (2000) the curve data are transformed by introducing two new parameters P (stimulation period) and u (transformed time):

$$P = 2 * max(t)$$

$$u = \sqrt{(2 * t * P)}$$

The new count values are then calculated by

$$ctsNEW = cts(u/P)$$

and the returned `data.frame` is produced by: `data.frame(u,ctsNEW)`

Value

The function returns the same data type as the input data type with the transformed curve values.

`data.frame`	generic R data structure
`RLum.Data.Curve`	package `RLum` `object`

Function version

0.4.1 (2015-03-04 18:47:17)

Note

The transformation is recommended for curves recorded with a channel resolution of at least 0.05 s/channel.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

Bulur, E., 2000. A simple transformation for converting CW-OSL curves to LM-OSL curves. Radiation Measurements, 32, 141-145.

Further Reading

Bulur, E., 1996. An Alternative Technique For Optically Stimulated Luminescence (OSL) Experiment. Radiation Measurements, 26, 701-709.

See Also

CW2pHMi, CW2pLMi, CW2pPMi, fit_LMCurve, lm, RLum.Data.Curve

The output of the function can be further used for LM-OSL fitting: CW2pLMi, CW2pHMi, CW2pPMi, fit_LMCurve, RLum.Data.Curve, plot_RLum

Examples

```
##read curve from CWOSL.SAR.Data transform curve and plot values
data(ExampleData.BINfileData, envir = environment())

##read id for the 1st OSL curve
id.OSL <- CWOSL.SAR.Data@METADATA[CWOSL.SAR.Data@METADATA[,"LTYPE"] == "OSL","ID"]

##produce x and y (time and count data for the data set)
x<-seq(CWOSL.SAR.Data@METADATA[id.OSL[1],"HIGH"]/CWOSL.SAR.Data@METADATA[id.OSL[1],"NPOINTS"],
       CWOSL.SAR.Data@METADATA[id.OSL[1],"HIGH"],
     by = CWOSL.SAR.Data@METADATA[id.OSL[1],"HIGH"]/CWOSL.SAR.Data@METADATA[id.OSL[1],"NPOINTS"])
y <- unlist(CWOSL.SAR.Data@DATA[id.OSL[1]])
values <- data.frame(x,y)

##transform values
values.transformed <- CW2pLM(values)

##plot
plot(values.transformed)
```

CW2pLMi *Transform a CW-OSL curve into a pLM-OSL curve via interpolation under linear modulation conditions*

Description

Transforms a conventionally measured continuous-wave (CW) OSL-curve into a pseudo linearly modulated (pLM) curve under linear modulation conditions using the interpolation procedure described by Bos & Wallinga (2012).

Usage

```
CW2pLMi(values, P)
```

Arguments

values	RLum.Data.Curve or data.frame (**required**): RLum.Data.Curve or data.frame with measured curve data of type stimulation time (t) (values[,1]) and measured counts (cts) (values[,2])
P	vector (optional): stimulation time in seconds. If no value is given the optimal value is estimated automatically (see details). Greater values of P produce more points in the rising tail of the curve.

Details

The complete procedure of the transformation is given in Bos & Wallinga (2012). The input data.frame consists of two columns: time (t) and count values (CW(t))

Nomenclature

P = stimulation time (s)
1/P = stimulation rate (1/s)

Internal transformation steps

(1) log(CW-OSL) values
(2) Calculate t' which is the transformed time:

$$t' = 1/2 * 1/P * t^2$$

(3) Interpolate CW(t'), i.e. use the log(CW(t)) to obtain the count values for the transformed time (t'). Values beyond min(t) and max(t) produce NA values.

(4) Select all values for t' < min(t), i.e. values beyond the time resolution of t. Select the first two values of the transformed data set which contain no NA values and use these values for a linear fit using lm.

(5) Extrapolate values for t' < min(t) based on the previously obtained fit parameters.

(6) Transform values using

$$pLM(t) = t/P * CW(t')$$

(7) Combine values and truncate all values for t' > `max(t)`

The number of values for t' < `min(t)` depends on the stimulation period (P) and therefore on the stimulation rate 1/P. To avoid the production of too many artificial data at the raising tail of the determined pLM curves it is recommended to use the automatic estimation routine for `P`*, i.e. provide no own value for* `P`.

Value

The function returns the same data type as the input data type with the transformed curve values.

`RLum.Data.Curve`
package `RLum` object with two additional info elements:

$CW2pLMi.x.t	: transformed time values
$CW2pLMi.method	: used method for the production of the new data points

Function version

0.3.1 (2015-03-04 18:48:02)

Note

According to Bos & Wallinga (2012) the number of extrapolated points should be limited to avoid artificial intensity data. If `P` is provided manually and more than two points are extrapolated, a warning message is returned.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne

Based on comments and suggestions from:
Adrie J.J. Bos, Delft University of Technology, The Netherlands

R Luminescence Package Team

References

Bos, A.J.J. & Wallinga, J., 2012. How to visualize quartz OSL signal components. Radiation Measurements, 47, 752-758.

Further Reading

Bulur, E., 1996. An Alternative Technique For Optically Stimulated Luminescence (OSL) Experiment. Radiation Measurements, 26, 701-709.

Bulur, E., 2000. A simple transformation for converting CW-OSL curves to LM-OSL curves. Radiation Measurements, 32, 141-145.

See Also

CW2pLM, CW2pHMi, CW2pPMi, fit_LMCurve, RLum.Data.Curve

Examples

```
##(1)
##load CW-OSL curve data
data(ExampleData.CW_OSL_Curve, envir = environment())

##transform values
values.transformed <- CW2pLMi(ExampleData.CW_OSL_Curve)

##plot
plot(values.transformed$x, values.transformed$y.t, log = "x")

##(2) - produce Fig. 4 from Bos & Wallinga (2012)
##load data
data(ExampleData.CW_OSL_Curve, envir = environment())
values <- CW_Curve.BosWallinga2012

##open plot area
plot(NA, NA,
     xlim = c(0.001,10),
     ylim = c(0,8000),
     ylab = "pseudo OSL (cts/0.01 s)",
     xlab = "t [s]",
     log = "x",
     main = "Fig. 4 - Bos & Wallinga (2012)")


values.t <- CW2pLMi(values, P = 1/20)
lines(values[1:length(values.t[,1]),1],CW2pLMi(values, P = 1/20)[,2],
      col = "red", lwd = 1.3)
text(0.03,4500,"LM", col = "red", cex = .8)

values.t <- CW2pHMi(values, delta = 40)
lines(values[1:length(values.t[,1]),1],CW2pHMi(values, delta = 40)[,2],
      col = "black", lwd = 1.3)
text(0.005,3000,"HM", cex =.8)

values.t <- CW2pPMi(values, P = 1/10)
lines(values[1:length(values.t[,1]),1], CW2pPMi(values, P = 1/10)[,2],
      col = "blue", lwd = 1.3)
text(0.5,6500,"PM", col = "blue", cex = .8)
```

CW2pPMi *Transform a CW-OSL curve into a pPM-OSL curve via interpolation under parabolic modulation conditions*

Description

Transforms a conventionally measured continuous-wave (CW) OSL-curve into a pseudo parabolic modulated (pPM) curve under parabolic modulation conditions using the interpolation procedure described by Bos & Wallinga (2012).

Usage

```
CW2pPMi(values, P)
```

Arguments

values	RLum.Data.Curve or data.frame (**required**): RLum.Data.Curve or data.frame with measured curve data of type stimulation time (t) (values[,1]) and measured counts (cts) (values[,2])
P	vector (optional): stimulation period in seconds. If no value is given, the optimal value is estimated automatically (see details). Greater values of P produce more points in the rising tail of the curve.

Details

The complete procedure of the transformation is given in Bos & Wallinga (2012). The input data.frame consists of two columns: time (t) and count values (CW(t))

Nomenclature

P = stimulation time (s)
1/P = stimulation rate (1/s)

Internal transformation steps

(1) log(CW-OSL) values

(2) Calculate t' which is the transformed time:

$$t' = (1/3) * (1/P^2)t^3$$

(3) Interpolate CW(t'), i.e. use the log(CW(t)) to obtain the count values for the transformed time (t'). Values beyond min(t) and max(t) produce NA values.

(4) Select all values for t' < min(t), i.e. values beyond the time resolution of t. Select the first two values of the transformed data set which contain no NA values and use these values for a linear fit using lm.

(5) Extrapolate values for t' < min(t) based on the previously obtained fit parameters. The extrapolation is limited to two values. Other values at the beginning of the transformed curve are set to 0.

(6) Transform values using

$$pLM(t) = t^2/P^2 * CW(t')$$

(7) Combine all values and truncate all values for t' > `max(t)`

The number of values for t' < `min(t)` depends on the stimulation period `P`. To avoid the production of too many artificial data at the raising tail of the determined pPM curve, it is recommended to use the automatic estimation routine for `P`, i.e. provide no value for `P`.

Value

The function returns the same data type as the input data type with the transformed curve values.

`RLum.Data.Curve`
package `RLum` `object` with two additional info elements:

$CW2pPMi.x.t	: transformed time values
$CW2pPMi.method	: used method for the production of the new data points

`data.frame` with four columns:

$x	: time
$y.t	: transformed count values
$x.t	: transformed time values
$method	: used method for the production of the new data points

Function version

0.2.1 (2015-03-04 18:48:47)

Note

According to Bos & Wallinga (2012), the number of extrapolated points should be limited to avoid artificial intensity data. If `P` is provided manually, not more than two points are extrapolated.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

Based on comments and suggestions from:
Adrie J.J. Bos, Delft University of Technology, The Netherlands

R Luminescence Package Team

References

Bos, A.J.J. & Wallinga, J., 2012. How to visualize quartz OSL signal components. Radiation Measurements, 47, 752-758.

Further Reading

Bulur, E., 1996. An Alternative Technique For Optically Stimulated Luminescence (OSL) Experiment. Radiation Measurements, 26, 701-709.

Bulur, E., 2000. A simple transformation for converting CW-OSL curves to LM-OSL curves. Radiation Measurements, 32, 141-145.

See Also

CW2pLM, CW2pLMi, CW2pHMi, fit_LMCurve, RLum.Data.Curve

Examples

```
##(1)
##load CW-OSL curve data
data(ExampleData.CW_OSL_Curve, envir = environment())

##transform values
values.transformed <- CW2pPMi(ExampleData.CW_OSL_Curve)

##plot
plot(values.transformed$x,values.transformed$y.t, log = "x")

##(2) - produce Fig. 4 from Bos & Wallinga (2012)

##load data
data(ExampleData.CW_OSL_Curve, envir = environment())
values <- CW_Curve.BosWallinga2012

##open plot area
plot(NA, NA,
     xlim = c(0.001,10),
     ylim = c(0,8000),
     ylab = "pseudo OSL (cts/0.01 s)",
     xlab = "t [s]",
     log = "x",
     main = "Fig. 4 - Bos & Wallinga (2012)")

values.t <- CW2pLMi(values, P = 1/20)
lines(values[1:length(values.t[,1]),1],CW2pLMi(values, P = 1/20)[,2],
      col = "red",lwd = 1.3)
text(0.03,4500,"LM", col = "red", cex = .8)

values.t <- CW2pHMi(values, delta = 40)
lines(values[1:length(values.t[,1]),1], CW2pHMi(values, delta = 40)[,2],
      col = "black", lwd = 1.3)
text(0.005,3000,"HM", cex = .8)

values.t <- CW2pPMi(values, P = 1/10)
lines(values[1:length(values.t[,1]),1], CW2pPMi(values, P = 1/10)[,2],
      col = "blue", lwd = 1.3)
text(0.5,6500,"PM", col = "blue", cex = .8)
```

ExampleData.BINfileData

Example data from a SAR OSL and SAR TL measurement for the package Luminescence

---

Description

Example data from a SAR OSL and TL measurement for package Luminescence directly extracted from a Risoe BIN-file and provided in an object of type Risoe.BINfileData-class

Usage

```
ExampleData.BINfileData
```

Format

`CWOSL.SAR.Data`: SAR OSL measurement data

`TL.SAR.Data`: SAR TL measurement data

Each class object contains two slots: (a) `METADATA` is a data.frame with all metadata stored in the BIN file of the measurements and (b) `DATA` contains a list of vectors of the measured data (usually count values).

Version

0.1

Source

CWOSL.SAR.Data

Lab:	Luminescence Laboratory Bayreuth
Lab-Code:	BT607
Location:	Saxony/Germany
Material:	Middle grain quartz measured on aluminum cups on a Risoe TL/OSL DA-15 reader
Reference:	unpublished

TL.SAR.Data

Lab:	Luminescence Laboratory of Cologne
Lab-Code:	LP1_5
Location:	Spain
Material:	Flint
Setup:	Risoe TL/OSL DA-20 reader (Filter: Semrock Brightline, HC475/50, N2, unpolished steel discs)
Reference:	unpublished
Remarks:	dataset limited to one position

References

CWOSL.SAR.Data: unpublished data

TL.SAR.Data: unpublished data

Examples

```
##show first 5 elements of the METADATA and DATA elements in the terminal
data(ExampleData.BINfileData, envir = environment())
CWOSL.SAR.Data@METADATA[1:5,]
CWOSL.SAR.Data@DATA[1:5]
```

ExampleData.CW_OSL_Curve

Example CW-OSL curve data for the package Luminescence

Description

`data.frame` containing CW-OSL curve data (time, counts)

Usage

```
data(ExampleData.CW_OSL_Curve)
```

Format

Data frame with 1000 observations on the following 2 variables:

`x` a numeric vector, time

`y` a numeric vector, counts

Details

see source

Source

ExampleData.CW_OSL_Curve

Lab:	Luminescence Laboratory Bayreuth
Lab-Code:	BT607
Location:	Saxony/Germany
Material:	Middle grain quartz measured on aluminum cups on a Risoe TL/OSL DA-15 reader.
Reference:	unpublished data

CW_Curve.BosWallinga2012

Lab:	Netherlands Centre for Luminescence Dating (NCL)
Lab-Code:	NCL-2108077
Location:	Guadalentin Basin, Spain
Material:	Coarse grain quartz
Reference:	Bos & Wallinga (2012) and Baartman et al. (2011)

References

Baartman, J.E.M., Veldkamp, A., Schoorl, J.M., Wallinga, J., Cammeraat, L.H., 2011. Unravelling Late Pleistocene and Holocene landscape dynamics: The Upper Guadalentin Basin, SE Spain.

Geomorphology, 125, 172-185.

Bos, A.J.J. & Wallinga, J., 2012. How to visualize quartz OSL signal components. Radiation Measurements, 47, 752-758.

Examples

```
data(ExampleData.CW_OSL_Curve, envir = environment())
plot(ExampleData.CW_OSL_Curve)
```

`ExampleData.DeValues` *Example De data sets for the package Luminescence*

Description

Equivalent dose (De) values measured for a fine grain quartz sample from a loess section in Rottewitz (Saxony/Germany) and for a coarse grain quartz sample from a fluvial deposit in the rock shelter of Cueva Anton (Murcia/Spain).

Usage

```
ExampleData.DeValues
```

Format

A `list` with two elements, each containing a two column `data.frame`:

`$BT998`: De and De error values for a fine grain quartz sample from a loess section in Rottewitz.

`$CA1`: Single grain De and De error values for a coarse grain quartz sample from a fluvial deposit in the rock shelter of Cueva Anton

Source

BT998

Lab:	Luminescence Laboratory Bayreuth
Lab-Code:	BT998
Location:	Rottewitz (Saxony/Germany)
Material:	Fine grain quartz measured on aluminum discs on a Risoe TL/OSL DA-15 reader
Units:	Values are given in seconds
Dose Rate:	Dose rate of the beta-source at measurement ca. 0.0438 Gy/s +/- 0.0019 Gy/s
Measurement Date:	2012-01-27

CA1

Lab:	Cologne Luminescence Laboratory (CLL)
Lab-Code:	C-L2941
Location:	Cueva Anton (Murcia/Spain)
Material:	Coarse grain quartz (200-250 microns) measured on single grain discs on a Risoe TL/OSL DA-20 r

Units:	Values are given in Gray
Measurement Date:	2012

References

BT998

Unpublished data

CA1

Burow, C., Kehl, M., Hilgers, A., Weniger, G.-C., Angelucci, D., Villaverde, V., Zapata, J. and Zilhao, J. (accepted). Luminescence dating of fluvial deposits in the rock shelter of Cueva Anton, Spain. Geochronometria.

Examples

```
##(1) plot values as histogram
data(ExampleData.DeValues, envir = environment())
plot_Histogram(ExampleData.DeValues$BT998, xlab = "De [s]")

##(2) plot value as histogram (with Second to Gray convertion)
data(ExampleData.DeValues, envir = environment())

De.values <- Second2Gray(ExampleData.DeValues$BT998,
                         dose.rate = c(0.0438, 0.0019),
                         method = "gaussian")

plot_Histogram(De.values, xlab = "De [Gy]")
```

ExampleData.FittingLM *Example data for fit_LMCurve() in the package Luminescence*

Description

Lineraly modulated (LM) measurement data from a quartz sample from Norway including background measurement. Measurements carried out in the luminescence laboratory at the University of Bayreuth.

Usage

```
ExampleData.FittingLM
```

Format

Two objects (data.frames) with two columns (time and counts).

Source

Lab:	Luminescence Laboratory Bayreuth
Lab-Code:	BT900
Location:	Norway
Material:	Beach deposit, coarse grain quartz measured on aluminum discs on a Risoe TL/OSL DA-15 reader

References

Fuchs, M., Kreutzer, S., Fischer, M., Sauer, D., Soerensen, R., 2012. OSL and IRSL dating of raised beach sand deposits along the southeastern coast of Norway. Quaternary Geochronology, 10, 195-200.

Examples

```
##show LM data
data(ExampleData.FittingLM, envir = environment())
plot(values.curve,log="x")
```

ExampleData.LxTxData *Example Lx/Tx data from CW-OSL SAR measurement*

Description

LxTx data from a SAR measurement for the package Luminescence.

Usage

```
ExampleData.LxTxData
```

Format

A `data.frame` with 4 columns (Dose, LxTx, LxTx.Error, TnTx).

Source

Lab:	Luminescence Laboratory Bayreuth
Lab-Code:	BT607
Location:	Ostrau (Saxony-Anhalt/Germany)
Material:	Middle grain (38-63 μm) quartz measured on a Risoe TL/OSL DA-15 reader.

References

unpublished data

Examples

```
##plot Lx/Tx data vs dose [s]
data(ExampleData.LxTxData, envir = environment())
plot(LxTxData$Dose,LxTxData$LxTx)
```

ExampleData.LxTxOSLData

Example Lx and Tx curve data from an artificial OSL measurement

---

Description

Lx and Tx data of continous wave (CW-) OSL signal curves.

Usage

```
ExampleData.LxTxOSLData.RData
```

Format

Two `data.frames` containing time and count values.

Source

Arbitrary OSL measurement.

References

unpublished data

Examples

```
##load data
data(ExampleData.LxTxOSLData, envir = environment())

##plot data
plot(Lx.data)
plot(Tx.data)
```

ExampleData.RLum.Analysis

Example data as `RLum.Analysis` objects

Description

Collection of different `RLum.Analysis` objects for protocol analysis.

Usage

```
ExampleData.RLum.Analysis
```

Format

IRSAR.RF.Data: IRSAR.RF.Data on coarse grain feldspar

Each object contains data needed for the given protocol analysis.

Version

0.1

Source

IRSAR.RF.Data

These data were kindly provided by Tobias Lauer and Matthias Krbetschek.

Lab:	Luminescence Laboratory TU Bergakademie Freiberg
Lab-Code:	ZEU/SA1
Location:	Zeuchfeld (Zeuchfeld Sandur; Saxony-Anhalt/Germany)
Material:	K-feldspar (130-200 μm)
Reference:	Kreutzer et al. (2014)

References

IRSAR.RF.Data

Kreutzer, S., Lauer, T., Meszner, S., Krbetschek, M.R., Faust, D., Fuchs, M., 2014. Chronology of the Quaternary profile Zeuchfeld in Saxony-Anhalt / Germany - a preliminary luminescence dating study. Zeitschrift fuer Geomorphologie 58, 5-26. doi: 10.1127/0372-8854/2012/S-00112

Examples

```
##load data
data(ExampleData.RLum.Analysis, envir = environment())

##plot data
plot_RLum(IRSAR.RF.Data)
```

ExampleData.RLum.Data.Image

Example data as RLum.Data.Image *objects*

Description

Measurement of Princton Instruments camera imported with the function readSPE2R to R to produce an RLum.Data.Image object.

Usage

```
ExampleData.RLum.Data.Image
```

Format

Object of class RLum.Data.Image

Version

0.1

Source

ExampleData.RLum.Data.Image

These data were kindly provided by Regina DeWitt.

Lab.:	Department of Physics, East-Carolina University, NC, USA
Lab-Code:	-
Location:	-
Material:	-
Reference:	-

Image data is a measurement of fluorescent ceiling lights with a cooled Princeton Instruments (TM) camera fitted on Risoe DA-20 TL/OSL reader.

References

-

Examples

```
##load data
data(ExampleData.RLum.Data.Image, envir = environment())

##plot data
plot_RLum(ExampleData.RLum.Data.Image)
```

ExampleData.XSYG *Example data for a SAR OSL measurement and a TL spectrum using a lexsyg reader*

Description

Example data from a SAR OSL measurement and a TL spectrum for package Luminescence imported from a Freiberg Instruments XSYG file using the function `readXSYG2R`.

Usage

```
ExampleData.XSYG
```

Format

`OSL.SARMeasurement`: SAR OSL measurement data

The data contain two elements: (a) `$Sequence.Header` is a data.frame with metadata from the measurement,(b) `Sequence.Object` contains an `RLum.Analysis` object for further analysis.

`TL.Spectrum`: TL spectrum data

RLum.Data.Spectrum object for further analysis. The spectrum was cleaned from cosmic-rays using the function apply_CosmicRayRemoval. Note that no quantum efficiency calibration was performed.

Version

0.1

Source

OSL.SARMeasurement

Lab:	Luminescence Laboratory Giessen
Lab-Code:	no code
Location:	not specified
Material:	Coarse grain quartz
	on steel cups on lexsyg research reader
Reference:	unpublished

TL.Spectrum

Lab:	Luminescence Laboratory Giessen
Lab-Code:	BT753
Location:	Dolni Vestonice/Czech Republic
Material:	Fine grain polymineral
	on steel cups on lexsyg rearch reader
Reference:	Fuchs et al., 2013
Spectrum:	Integration time 19 s, channel time 20 s
Heating:	1 K/s, up to 500 deg. C

References

Unpublished data measured to serve as example data for that package. Location origin of sample BT753 is given here:

Fuchs, M., Kreutzer, S., Rousseau, D.D., Antoine, P., Hatte, C., Lagroix, F., Moine, O., Gauthier, C., Svoboda, J., Lisa, L., 2013. The loess sequence of Dolni Vestonice, Czech Republic: A new OSL-based chronology of the Last Climatic Cycle. Boreas, 42, 664–677.

See Also

readXSYG2R, RLum.Analysis, RLum.Data.Spectrum, plot_RLum, plot_RLum.Analysis, plot_RLum.Data.Spectrum

Examples

```
##show data
data(ExampleData.XSYG, envir = environment())

## ========================================
##(1) OSL.SARMeasurement
OSL.SARMeasurement

##show $Sequence.Object
```

```
OSL.SARMeasurement$Sequence.Object

##grep OSL curves and plot the first curve
OSLcurve <- get_RLum.Analysis(OSL.SARMeasurement$Sequence.Object,
recordType="OSL")[[1]]
plot_RLum(OSLcurve)

## ========================================
##(2) TL.Spectrum
TL.Spectrum

##plot simple spectrum (2D)
plot_RLum.Data.Spectrum(TL.Spectrum,
                        plot.type="contour",
                        xlim = c(310,750),
                        ylim = c(0,300),
                        bin.rows=10,
                        bin.cols = 1)

##plot 3d spectrum (uncomment for usage)
# plot_RLum.Data.Spectrum(TL.Spectrum, plot.type="persp",
# xlim = c(310,750), ylim = c(0,300), bin.rows=10,
# bin.cols = 1)
```

`extract_IrradiationTimes` *Extract irradiation times from an XSYG file*

Description

Extracts irradiation times, dose and times since last irradiation, from a Freiberg Instruments XSYG-file. These information can be further used to update an existing BINX-file

Usage

```
extract_IrradiationTimes(file.XSYG, file.BINX, recordType = c("irradiation (NA)",
    "IRSL (UVVIS)", "OSL (UVVIS)", "TL (UVVIS)"), txtProgressBar = TRUE)
```

Arguments

`file.XSYG`	`character` (**required**): path and file name of the XSYG file.
`file.BINX`	`character` (optional): path and file name of an existing BINX-file. If a file name is provided the file will be updated with the information from the XSYG file in the same folder as the original BINX-file. Note: The XSYG and the BINX-file have to be originate from the same measurement!
`recordType`	`character` (with default): select relevant curves types from the XSYG file. As the XSYG-file format comprises much more information than usually needed for routine data analysis and allowed in the BINX-file format, only the relevant

curves are selected by using the function get_RLum.Analysis. The argument recordType works as described for this function.

Note: A wrong selection will causes a function error. Please change this argument only if you have reasons to do so.

txtProgressBar logical (with default): enables TRUE or disables FALSE the progression bars during import and export

Details

The function was written to compensate missing information in the BINX-file output of Freiberg Instruments lexsyg readers. As all information are available within the XSYG-file anyway, these information can be extracted and used for further analysis or/and to stored in a new BINX-file, which can be further used by other software, e.g. Analyst (Geoff Duller).

Typical application example: g-value estimation from fading measurements using the Analyst or any other self written script.

Beside the some simple data transformation steps the function applies the functions readXSYG2R, readBIN2R, writeR2BIN for data import and export.

Value

An RLum.Results object is returned with the following structure:
.. $irr.times (data.frame)

If a BINX-file path and name is set, the output will be additionally transferred to a new BINX-file with the function name as suffix. For the output the path of the input BINX-file itself is used.

Function version

0.1 (2015-03-23 12:56:18)

Note

The produced output object contains still the irradiation steps to keep the output transparent. However, for the BINX-file export this steps are removed as the BINX-file format description does not allow irradiations as separat sequences steps.

Know issue: The 'fading correction' menu in the Analyst will not work appear with the produced BIN/BINX-file due to hidden bits, which are not reproduced by the function writeR2BIN().

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

Duller, G., 2007. Analyst.

See Also

RLum.Results, Risoe.BINfileData, readXSYG2R, readBIN2R, writeR2BIN

Examples

```
## (1) - example for your own data
##
## set files and run function
#
#   file.XSYG <- file.choose()
#   file.BINX <- file.choose()
#
#     output <- extract_IrradiationTimes(file.XSYG = file.XSYG, file.BINX = file.BINX)
#     get_RLum.Results(output)
#
## export results additionally to a CSV.file in the same directory as the XSYG-file
#       write.table(x = get_RLum.Results(output),
#                   file = paste0(file.BINX,"_extract_IrradiationTimes.csv"),
#                   sep = ";",
#                   row.names = FALSE)
```

---

fit_CWCurve *Nonlinear Least Squares Fit for CW-OSL curves [beta version]*

Description

The function determines the weighted least-squares estimates of the component parameters of a CW-OSL signal for a given maximum number of components and returns various component parameters. The fitting procedure uses the nls function with the port algorithm.

Usage

```
fit_CWCurve(values, n.components.max, fit.failure_threshold = 3,
    fit.trace = FALSE, fit.calcError = FALSE, LED.power = 36,
    LED.wavelength = 470, cex.global = 0.6, sample_code = "Default",
    output.path, output.terminal = TRUE, output.terminalAdvanced = TRUE,
    output.plot = TRUE, ...)
```

Arguments

values	RLum.Data.Curve or data.frame (**required**): x, y data of measured values (time and counts). See examples.
n.components.max	vector (optional): maximum number of components that are to be used for fitting. The upper limit is 7.
fit.failure_threshold	vector (with default): limits the failed fitting attempts.
fit.trace	logical (with default): traces the fitting process on the terminal.
fit.calcError	logical (with default): calculate 1-sigma error range of components using confint

`LED.power`	numeric (with default): LED power (max.) used for intensity ramping in mW/cm^2. **Note:** The value is used for the calculation of the absolute photoionisation cross section.
`LED.wavelength`	numeric (with default): LED wavelength used for stimulation in nm. **Note:** The value is used for the calculation of the absolute photoionisation cross section.
`cex.global`	numeric (with default): global scaling factor.
`sample_code`	character (optional): sample code used for the plot and the optional output table (mtext).
`output.path`	character (optional): output path for table output containing the results of the fit. The file name is set automatically. If the file already exists in the directory, the values are appended.
`output.terminal`	logical (with default): terminal ouput with fitting results.
`output.terminalAdvanced`	logical (with default): enhanced terminal output. Requires `output.terminal = TRUE`. If `output.terminal = FALSE` no advanced output is possible.
`output.plot`	logical (with default): returns a plot of the fitted curves.
`...`	further arguments and graphical parameters passed to `plot`.

Details

Fitting function

The function for the CW-OSL fitting has the general form:

$$y = I0_1 * \lambda_1 * exp(-\lambda_1 * x) + , \ldots , + I0_i * \lambda_i * exp(-\lambda_i * x)$$

where $1 < i < 8$

and λ is the decay constant and $N0$ the intial number of trapped electrons.
(for the used equation cf. Boetter-Jensen et al., 2003)

Start values

Start values are estimated automatically by fitting a linear function to the logarithmized input data set. Currently, there is no option to manually provide start parameters.

Goodness of fit

The goodness of the fit is given as pseudoR^2 value (pseudo coefficient of determination). According to Lave (1970), the value is calculated as:

$$pseudoR^2 = 1 - RSS/TSS$$

where $RSS = Residual\ Sum\ of\ Squares$
and $TSS = Total\ Sum\ of\ Squares$

Error of fitted component parameters

The 1-sigma error for the components is calculated using the function confint. Due to considerable calculation time, this option is deactived by default. In addition, the error for the components can be estimated by using internal R functions like summary. See the nls help page for more information.

For details on the nonlinear regression in R, see Ritz & Streibig (2008).

Value

plot (optional) the fitted CW-OSL curves are returned as plot.

table (optional) an output table (*.csv) with parameters of the fitted components is provided if the output.path is set.

RLum.Results object
beside the plot and table output options, an RLum.Results object is returned.

fit: an nls object ($fit) for which generic R functions are provided, e.g. summary, confint, profile. For more details, see nls.

output.table: a data.frame containing the summarised parameters including the error
component.contribution.matrix: matrix containing the values for the component to sum contribution plot ($component.contribution.matrix).

Matrix structure:
Column 1 and 2: time and rev(time) values
Additional columns are used for the components, two for each component, containing I0 and n0. The last columns cont. provide information on the relative component contribution for each time interval including the row sum for this values.

Function version

0.4.4 (2015-03-04 00:19:53)

Note

Beta version - This function has not been properly tested yet and should therefore not be used for publication purposes!

The pseudo-R^2 may not be the best parameter to describe the goodness of the fit. The trade off between the n.components and the pseudo-R^2 value is currently not considered.

The function **does not** ensure that the fitting procedure has reached a global minimum rather than a local minimum!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
R Luminescence Package Team

References

Boetter-Jensen, L., McKeever, S.W.S., Wintle, A.G., 2003. Optically Stimulated Luminescence Dosimetry. Elsevier Science B.V.

Lave, C.A.T., 1970. The Demand for Urban Mass Transportation. The Review of Economics and Statistics, 52 (3), 320-323.

Ritz, C. & Streibig, J.C., 2008. Nonlinear Regression with R. In: R. Gentleman, K. Hornik, G. Parmigiani, eds., Springer, p. 150.

See Also

fit_LMCurve, plot,nls, RLum.Data.Curve, RLum.Results, get_RLum.Results

Examples

```
##load data
data(ExampleData.CW_OSL_Curve, envir = environment())

##fit data
fit <- fit_CWCurve(values = ExampleData.CW_OSL_Curve,
                   main = "CW Curve Fit",
                   n.components.max = 4,
                   log = "x")
```

---

fit_LMCurve *Nonlinear Least Squares Fit for LM-OSL curves*

Description

The function determines weighted nonlinear least-squares estimates of the component parameters of an LM-OSL curve (Bulur 1996) for a given number of components and returns various component parameters. The fitting procedure uses the function nls with the port algorithm.

Usage

```
fit_LMCurve(values, values.bg, n.components = 3, start_values,
    input.dataType = "LM", sample_code = "", sample_ID = "",
    LED.power = 36, LED.wavelength = 470, cex.global = 0.8, fit.trace = FALSE,
    fit.advanced = FALSE, fit.calcError = FALSE, bg.subtraction = "polynomial",
    output.path, output.terminal = TRUE, output.terminaladvanced = TRUE,
    output.plot = TRUE, output.plotBG = FALSE, ...)
```

Arguments

values	RLum.Data.Curve or data.frame (**required**): x,y data of measured values (time and counts). See examples.
values.bg	RLum.Data.Curve or data.frame (optional): x,y data of measured values (time and counts) for background subtraction.
n.components	integer (with default): fixed number of components that are to be recognised during fitting (min = 1, max = 7).

`start_values`	data.frame (optional): start parameters for lm and xm data for the fit. If no start values are given, an automatic start value estimation is attempted (see details).
`input.dataType`	character (with default): alter the plot output depending on the input data: "LM" or "pLM" (pseudo-LM). See: CW2pLM
`sample_code`	character (optional): sample code used for the plot and the optional output table (mtext).
`sample_ID`	character (optional): additional identifier used as column header for the table output.
`LED.power`	numeric (with default): LED power (max.) used for intensity ramping in mW/cm^2. **Note:** This value is used for the calculation of the absolute photoionisation cross section.
`LED.wavelength`	numeric (with default): LED wavelength in nm used for stimulation. **Note:** This value is used for the calculation of the absolute photoionisation cross section.
`cex.global`	numeric (with default): global scaling factor.
`fit.trace`	logical (with default): traces the fitting process on the terminal.
`fit.advanced`	logical (with default): enables advanced fitting attempt for automatic start parameter recognition. Works only if no start parameters are provided. **Note:** It may take a while.
`fit.calcError`	logical (with default): calculate 1-sigma error range of components using confint.
`bg.subtraction`	character (with default): specifies method for background subtraction (`polynomial`, `linear`, `channel`, see Details). **Note:** requires input for `values.bg`.
`output.path`	character (optional): output path for table output containing the results of the fit. The file name is set automatically. If the file already exists in the directory, the values are appended.
`output.terminal`	logical (with default): terminal output with fitting results.
`output.terminaladvanced`	logical (with default): enhanced terminal output. Requires `output.terminal = TRUE`. If `output.terminal = FALSE` no advanced output is possible.
`output.plot`	logical (with default): returns a plot of the fitted curves.
`output.plotBG`	logical (with default): returns a plot of the background values with the fit used for the background subtraction.
`...`	Further arguments that may be passed to the plot output, e.g. `xlab`, `xlab`, `main`, `log`.

Details

Fitting function

The function for the fitting has the general form:

$$y = (exp(0.5)*Im_1*x/xm_1)*exp(-x^2/(2*xm_1^2))+,\ldots,+exp(0.5)*Im_i*x/xm_i)*exp(-x^2/(2*xm_i^2))$$

where $1 < i < 8$
This function and the equations for the conversion to b (detrapping probability) and n0 (proportional to initially trapped charge) have been taken from Kitis et al. (2008):

$$xm_i = \sqrt{max(t)/b_i}$$

$$Im_i = exp(-0.5)n0/xm_i$$

Background subtraction

Three methods for background subtraction are provided for a given background signal (`values.bg`). `polynomial`: default method. A polynomial function is fitted using glm and the resulting function is used for background subtraction:

$$y = a * x^4 + b * x^3 + c * x^2 + d * x + e$$

`linear`: a linear function is fitted using glm and the resulting function is used for background subtraction:

$$y = a * x + b$$

`channel`: the measured background signal is subtracted channelwise from the measured signal.

Start values

The choice of the initial parameters for the `nls`-fitting is a crucial point and the fitting procedure may mainly fail due to ill chosen start parameters. Here, three options are provided:

(a) If no start values (`start_values`) are provided by the user, a cheap guess is made by using the detrapping values found by Jain et al. (2003) for quartz for a maximum of 7 components. Based on these values, the pseudo start parameters xm and Im are recalculated for the given data set. In all cases, the fitting starts with the ultra-fast component and (depending on `n.components`) steps through the following values. If no fit could be achieved, an error plot (for `output.plot = TRUE`) with the pseudo curve (based on the pseudo start parameters) is provided. This may give the opportunity to identify appropriate start parameters visually.

(b) If start values are provided, the function works like a simple `nls` fitting approach.

(c) If no start parameters are provided and the option `fit.advanced = TRUE` is chosen, an advanced start paramter estimation is applied using a stochastical attempt. Therefore, the recalculated start parameters **(a)** are used to construct a normal distribution. The start parameters are then sampled randomly from this distribution. A maximum of 100 attempts will be made. **Note:** This process may be time consuming.

Goodness of fit

The goodness of the fit is given by a pseudoR^2 value (pseudo coefficient of determination). According to Lave (1970), the value is calculated as:

$$pseudoR^2 = 1 - RSS/TSS$$

where $RSS = Residual\ Sum\ of\ Squares$
and $TSS = Total\ Sum\ of\ Squares$

Error of fitted component parameters

The 1-sigma error for the components is calculated using the function confint. Due to considerable calculation time, this option is deactived by default. In addition, the error for the components

can be estimated by using internal R functions like summary. See the nls help page for more information.
For more details on the nonlinear regression in R, see Ritz & Streibig (2008).

Value

`plot` (optional) various types of plots are returned. For details see above.

`table` (optional) an output table (*.csv) with the fitted components is provided if the `output.path` is set.

`list object` beside the plot and table output, a list is returned. The list contains:
(a) an `nls` object (`$fit`) for which generic R functions are provided, e.g. summary, confint, profile. For more details, see nls.
(b) a data.frame containing the summarised parameters including the error (`$output.table`).
(c) a matrix containing the values for the component to sum contribution plot (`$component.contribution.matrix`).

Matrix structure:
Column 1 and 2: time and `rev(time)` values
Additional columns are used for the components, two for each component, containing I0 and n0. The last columns `cont.` provide information on the relative component contribution for each time interval including the row sum for this values.

Function version

0.2.16 (2015-03-10 16:11:27)

Note

The pseudo-R^2 may not be the best parameter to describe the goodness of the fit. The trade off between the `n.components` and the pseudo-R^2 value currently remains unconsidered.

The function **does not** ensure that the fitting procedure has reached a global minimum rather than a local minimum! In any case of doubt, the use of manual start values is highly recommended.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

Bulur, E., 1996. An Alternative Technique For Optically Stimulated Luminescence (OSL) Experiment. Radiation Measurements, 26, 5, 701-709.

Jain, M., Murray, A.S., Boetter-Jensen, L., 2003. Characterisation of blue-light stimulated luminescence components in different quartz samples: implications for dose measurement. Radiation Measurements, 37 (4-5), 441-449.

Kitis, G. & Pagonis, V., 2008. Computerized curve deconvolution analysis for LM-OSL. Radiation Measurements, 43, 737-741.

Lave, C.A.T., 1970. The Demand for Urban Mass Transportation. The Review of Economics and Statistics, 52 (3), 320-323.

Ritz, C. & Streibig, J.C., 2008. Nonlinear Regression with R. R. Gentleman, K. Hornik, & G. Parmigiani, eds., Springer, p. 150.

See Also

fit_CWCurve, plot, nls

Examples

```
##(1) fit LM data without background subtraction
data(ExampleData.FittingLM, envir = environment())
fit_LMCurve(values = values.curve, n.components = 3, log = "x")

##(2) fit LM data with background subtraction and export as JPEG
## -alter file path for your preferred system
##jpeg(file = "~/Desktop/Fit_Output\%03d.jpg", quality = 100,
## height = 3000, width = 3000, res = 300)
data(ExampleData.FittingLM, envir = environment())
fit_LMCurve(values = values.curve, values.bg = values.curveBG,
            n.components = 2, log = "x", output.plotBG = TRUE)
##dev.off()

##(3) fit LM data with manual start parameters
data(ExampleData.FittingLM, envir = environment())
fit_LMCurve(values = values.curve,
            values.bg = values.curveBG,
            n.components = 3,
            log = "x",
            start_values = data.frame(Im = c(170,25,400), xm = c(56,200,1500)))
```

---

get_Layout *Collection of layout definitions*

Description

This helper function returns a list with layout definitions for homogeneous plotting.

Usage

```
get_Layout(layout)
```

Arguments

layout	character or list object (required): name of the layout definition to be returned. If name is provided the respective definition is returned. One of the following supported layout definitions is possible: "default", "journal.1", "small", "empty". User-specific layout definitions must be provided as a list object of predefined structure, see details.

Details

The easiest way to create a user-specific layout definition is perhaps to create either an empty or a default layout object and fill/modify the definitions (`user.layout <-get_Layout(data = "empty")`).

Value

A list object with layout definitions for plot functions.

Function version

0.1 (2015-03-04 00:19:53)

Author(s)

Michael Dietze, GFZ Potsdam (Germany)
R Luminescence Package Team

Examples

```
## read example data set
data(ExampleData.DeValues, envir = environment())

## show structure of the default layout definition
layout.default <- get_Layout(layout = "default")
str(layout.default)

## show colour definitions for Abanico plot, only
layout.default$abanico$colour

## set Abanico plot title colour to orange
layout.default$abanico$colour$main <- "orange"

## create Abanico plot with modofied layout definition
plot_AbanicoPlot(data = ExampleData.DeValues,
                 layout = layout.default)

## create Abanico plot with predefined layout "journal"
plot_AbanicoPlot(data = ExampleData.DeValues,
                 layout = "journal")
```

---

get_RLum *General accessor function for RLum S4 class objects*

Description

Function calls object-specific get functions for RLum S4 class objects.

Usage

```
get_RLum(object, ...)
```

Arguments

object	RLum (**required**): S4 object of class RLum
...	further arguments that one might want to pass to the specific get function

Details

The function provides a generalised access point for specific RLum objects.
Depending on the input object, the corresponding get function will be selected. Allowed arguments can be found in the documentations of each get function.

object		corresponding get function
RLum.Data.Curve	:	get_RLum.Data.Curve
RLum.Data.Image	:	get_RLum.Data.Image
RLum.Data.Spectrum	:	get_RLum.Data.Spectrum
RLum.Analysis	:	get_RLum.Analysis
RLum.Results	:	get_RLum.Results

Value

Return is the same as input objects as provided in the list.

Function version

0.1 (2015-03-04 14:39:52)

Note

-

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

-

See Also

get_RLum.Data.Curve, RLum.Data.Curve, get_RLum.Data.Image, RLum.Data.Image, get_RLum.Data.Spectrum, RLum.Data.Spectrum, get_RLum.Analysis, RLum.Analysis, get_RLum.Results, RLum.Results

Examples

```
##Example based using data and from the calc_CentralDose() function

##load example data
data(ExampleData.DeValues, envir = environment())

##apply the central dose model 1st time
temp1 <- calc_CentralDose(ExampleData.DeValues$CA1)
```

```
##get results and store them in a new object
temp.get<- get_RLum(object = temp1)
```

`merge_Risoe.BINfileData` *Merge Risoe.BINfileData objects or Risoe BIN-files*

Description

Function allows merging Risoe BIN/BINX files or Risoe.BINfileData objects.

Usage

```
merge_Risoe.BINfileData(input.objects, output.file, keep.position.number = FALSE,
    position.number.append.gap = 0)
```

Arguments

`input.objects`	`character` or `Risoe.BINfileData` (**required**): Character vector with path and files names (e.g. `input.objects = c("path/file1.bin", "path/file2.bin")`) or `Risoe.BINfileData` objects (e.g. `input.objects = c(object1, object2)`)
`output.file`	`character` (optional): File output path and name. If no value is given, a `Risoe.BINfileData` is returned instead of a file.
`keep.position.number`	`logical` (with default): Allows keeping the original position numbers of the input objects. Otherwise the position numbers are recalculated.
`position.number.append.gap`	`integer` (with default): Set the position number gap between merged BIN-file sets, if the option `keep.position.number = FALSE` is used. See details for further information.

Details

The function allows merging different measurements to one file or one object.
The record IDs are recalculated for the new object. Other values are kept for each object. The number of input objects is not limited.

`position.number.append.gap` option

If the option `keep.position.number = FALSE` is used, the position numbers of the new data set are recalculated by adding the highest position number of the previous data set to the each position number of the next data set. For example: The highest position number is 48, then this number will be added to all other position numbers of the next data set (e.g. 1 + 48 = 49)

However, there might be cases where an additional addend (summand) is needed before the next position starts. Example:

Position number set (A): `1,3,5,7`
Position number set (B): `1,3,5,7`

With no additional summand the new position numbers would be: `1,3,5,7,8,9,10,11`. That might be unwanted. Using the argument `position.number.append.gap = 1` it will become: `1,3,5,7,9,11,13,15,17`.

Value

Returns a `file` or a `Risoe.BINfileData` object.

Function version

0.2.2 (2015-03-04 12:43:39)

Note

The validity of the output objects is not further checked.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

Duller, G., 2007. Analyst.

See Also

`Risoe.BINfileData`, `readBIN2R`, `writeR2BIN`

Examples

```
##merge two objects
data(ExampleData.BINfileData, envir = environment())

object1 <- CWOSL.SAR.Data
object2 <- CWOSL.SAR.Data

object.new <- merge_Risoe.BINfileData(c(object1, object2))
```

merge_RLum *General merge function for RLum S4 class objects*

Description

Function calls object-specific merge functions for RLum S4 class objects.

Usage

```
merge_RLum(objects, ...)
```

Arguments

objects	list of RLum (**required**): list of S4 object of class RLum
...	further arguments that one might want to pass to the specific merge function

Details

The function provides a generalised access point for merge specific RLum objects.
Depending on the input object, the corresponding merge function will be selected. Allowed arguments can be found in the documentations of each merge function.

object		corresponding merge function
RLum.Results	:	merge_RLum.Results

Value

Return is the same as input objects as provided in the list.

Function version

0.1 (2015-03-04 14:47:38)

Note

So far not for every RLum object a merging function exists.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

#

See Also

merge_RLum.Results, RLum.Results,

Examples

```
##Example based using data and from the calc_CentralDose() function

##load example data
data(ExampleData.DeValues, envir = environment())

##apply the central dose model 1st time
temp1 <- calc_CentralDose(ExampleData.DeValues$CA1)

##apply the central dose model 2nd time
temp2 <- calc_CentralDose(ExampleData.DeValues$CA1)

##merge the results and store them in a new object
temp.merged <- get_RLum.Results(merge_RLum(objects = list(temp1, temp2)))
```

---

merge_RLum.Analysis *Merge function for RLum.Analysis S4 class objects*

Description

Function allows merging of RLum.Analysis objects and adding of allowed objects to an RLum.Analysis.

Usage

```
merge_RLum.Analysis(objects)
```

Arguments

objects	list of RLum.Analysis (**required**): list of S4 objects of class RLum.Analysis. Furthermore other objects of class RLum can be added, see details.

Details

This function simply allowing to merge RLum.Analysis objects. Additionally other RLum objects can be added to an existing RLum.Analysis object. Supported objects to be added are: RLum.Data.Curve, RLum.Data.Spectrum and RLum.Data.Image.

The order in the new RLum.Analysis object is the object order provided with the input list.

Value

Return an RLum.Analysis object.

Function version

0.1 (2015-03-04 00:19:53)

Note

The information for the slot 'protocol' is taken from the first RLum.Analysis object in the input list. Therefore at least one object of type RLum.Analysis has to be provided.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

-

See Also

merge_RLum, RLum.Analysis, RLum.Data.Curve, RLum.Data.Spectrum, RLum.Data.Image, RLum

Examples

```
##merge different RLum objects from the example data
data(ExampleData.RLum.Analysis, envir = environment())
data(ExampleData.BINfileData, envir = environment())

object <- Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos=1)
curve <- get_RLum(object)[[2]]

temp.merged <- merge_RLum.Analysis(list(curve, IRSAR.RF.Data, IRSAR.RF.Data))
```

---

merge_RLum.Data.Curve *Merge function for RLum.Data.Curve S4 class objects*

Description

Function allows merging of RLum.Data.Curve objects in different ways

Usage

```
merge_RLum.Data.Curve(object, merge.method = "mean", method.info)
```

Arguments

object	list of RLum.Data.Curve (**required**): list of S4 objects of class RLum.Curve.
merge.method	character (**required**): method for combining of the objects, e.g. 'mean', 'sum', see details for further information and allowed methods. Note: Elements in slot info will be taken from the first curve in the list.
method.info	numeric (optional): allows to specify how info elements of the input objects are combined, e.g. 1 means that just the elements from the first object are kept, 2 keeps only the info elements from the 2 object etc. If nothing is provided all elements are combined.

Details

This function simply allowing to merge RLum.Data.Curve objects without touching the objects itself. Merging is always applied on the 2nd colum of the data matrix of the object.

Supported merge operations are RLum.Data.Curve

"sum"

All count values will be summed up using the function rowSums.

"mean"

The mean over the count values is calculated using the function rowMeans.

"-"

The row sums of the last objects are subtracted from the first object.

"*"

The row sums of the last objects are mutliplied with the first object.

"/"

Values of the first object are divided by row sums of the last objects.

Value

Return an RLum.Data.Curve object.

Function version

0.1 (2015-03-04 00:19:53)

Note

The information from the slot 'recordType' is taken from the first RLum.Data.Curve object in the input list. The slot 'curveType' is filled with the name merged.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

-

See Also

merge_RLum, RLum.Data.Curve

Examples

```
##load example data
data(ExampleData.XSYG, envir = environment())

##grep first and 3d TL curves
TL.curves  <- get_RLum.Analysis(OSL.SARMeasurement$Sequence.Object, recordType = "TL (UVVIS)")
TL.curve.1 <- TL.curves[[1]]
TL.curve.3 <- TL.curves[[3]]

##plot single curves
plot_RLum(TL.curve.1)
plot_RLum(TL.curve.3)

##subtract the 1st curve from the 2nd and plot
TL.curve.merged <- merge_RLum.Data.Curve(list(TL.curve.3, TL.curve.1), merge.method = "/")
plot_RLum(TL.curve.merged)
```

---

plot_AbanicoPlot *Function to create an Abanico Plot.*

Description

A plot is produced which allows comprehensive presentation of data precision and its dispersion around a central value as well as illustration of a kernel density estimate of the dose values.

Usage

```
plot_AbanicoPlot(data, na.exclude = TRUE, log.z = TRUE, central.value,
    centrality = "mean.weighted", dispersion = "sd", plot.ratio = 0.75,
    rotate = FALSE, mtext, summary, summary.pos, legend, legend.pos,
    stats, rug = FALSE, kde = TRUE, hist = FALSE, dots = FALSE,
    y.axis = TRUE, error.bars = FALSE, polygon.col, bar.col,
    line, line.col, line.label, grid.col, bw = "SJ", output = FALSE,
    ...)
```

Arguments

data	data.frame or RLum.Results object (required): for data.frame two columns: De (data[,1]) and De error (data[,2]). To plot several data sets in one plot the data sets must be provided as list, e.g. list(data.1, data.2).
na.exclude	logical (with default): exclude NA values from the data set prior to any further operations.
log.z	logical (with default): Option to display the z-axis in logarithmic scale. Default is TRUE.
central.value	numeric: User-defined central value, primarily used for horizontal centering of the z-axis.

`centrality` character or numeric (with default): measure of centrality, used for automatically centering the plot and drawing the central line. Can either be one out of `"mean"`, `"median"`, `"mean.weighted"` and `"median.weighted"` or one or more numeric values used for the standardisation. If more than one value is specified, more than one 2-sigma bar will be plotted and the dataset is centered using the median. Default is `"mean.weighted"`.

`dispersion` character (with default): measure of dispersion, used for drawing the polygon that depicts the dose distribution. One out of `"sd"` (standard deviation),`"2sd"` (2 standard deviations), `"qr"` (quartile range) or `"cinn"` (confidence interval with nn specifying the level, e.g. `"ci95"` meaning the 95 % confidence interval, i.e. data between the quantiles 0.025 and 0.975), default is `"sd"`.

`plot.ratio` numeric: Relative space, given to the radial versus the cartesian plot part, deault is `0.75`.

`rotate` logical: Option to turn the plot by 90 degrees.

`mtext` character: additional text below the plot title.

`summary` character (optional): adds numerical output to the plot. Can be one or more out of: `"n"` (number of samples), `"mean"` (mean De value), `"mean.weighted"` (error-weighted mean), `"median"` (median of the De values), `"sdrel"` (relative standard deviation in percent), `"sdabs"` (absolute standard deviation), `"serel"` (relative standard error), `"seabs"` (absolute standard error) and `"in.ci"` (percent of samples in confidence interval, e.g. 2-sigma).

`summary.pos` numeric or character (with default): optional position coordinates or keyword (e.g. `"topright"`) for the statistical summary. Alternatively, the keyword `"sub"` may be specified to place the summary below the plot header. However, this latter option in only possible if `mtext` is not used.

`legend` character vector (optional): legend content to be added to the plot.

`legend.pos` numeric or character (with default): optional position coordinates or keyword (e.g. `"topright"`) for the legend to be plotted.

`stats` character: additional labels of statistically important values in the plot. One or more out of the following: `"min"`, `"max"`, `"median"`.

`rug` logical: Option to add a rug to the KDE part, to indicate the location of individual values.

`kde` logical: Option to add a KDE plot to the dispersion part, default is `TRUE`.

`hist` logical: Option to add a histogram to the dispersion part. Only meaningful when not more than one data set is plotted.

`dots` logical: Option to add a dot plot to the dispersion part. If number of dots exceeds space in the dispersion part, a square indicates this.

`y.axis` logical: Option to hide y-axis labels. Useful for data with small scatter.

`error.bars` logical: Option to show De-errors as error bars on De-points. Useful in combination with `y.axis = FALSE, bar.col = "none"`.

`polygon.col` character or numeric (with default): colour of the polygon showing the dose dispersion around the central value. To disable the polygon use `"none"`. Default is `"grey80"`.

`bar.col` character or numeric (with default): colour of the bar showing the 2-sigma range of the dose error around the central value. To disable the bar use `"none"`. Default is `"grey50"`.

`line` numeric: numeric values of the additional lines to be added.

line.col	character or numeric: colour of the additional lines.
line.label	character: labels for the additional lines.
grid.col	character or numeric (with default): colour of the grid lines (originating at [0,0] and strechting to the z-scale). To disable grid lines use "none". Default is "grey".
bw	character (with default): bin-width for KDE, choose a numeric value for manual setting.
output	logical: Optional output of numerical plot parameters. These can be useful to reproduce similar plots. Default is FALSE.
...	Further plot arguments to pass. xlab must be a vector of length 2, specifying the upper and lower x-axes labels.

Details

The Abanico Plot is a combination of the classic Radial Plot (plot_RadialPlot) and a kernel density estimate plot (e.g. plot_KDE). It allows straightforward visualisation of data precision, error scatter around a user-defined central value and the combined distribution of the values, on the actual scale of the measured data (e.g. seconds, equivalent dose, years). The principle of the plot is shown in Galbraith & Green (1990). The function authors are thankful for the thoughtprovocing figure in this article.
The semi circle (z-axis) of the classic Radial Plot is bent to a straight line here, which actually is the basis for combining this polar (radial) part of the plot with any other cartesian visualisation method (KDE, histogram, PDF and so on). Note that the plot allows dispaying two measures of distribution. One is the 2-sigma bar, which illustrates the spread in value errors, and the other is the polygon, which stretches over both parts of the Abanico Plot (polar and cartesian) and illustrates the actual spread in the values themselfes.
Since the 2-sigma-bar is a polygon, it can be (and is) filled with shaded lines. To change density (lines per inch, default is 15) and angle (default is 45 degrees) of the shading lines, specify these parameters. See ?polygon() for further help.
The Abanico Plot supports other than the weighted mean as measure of centrality. When it is obvious that the data is not (log-)normally distributed, the mean (weighted or not) cannot be a valid measure of centrality and hence central dose. Accordingly, the median and the weighted median can be chosen as well to represent a proper measure of centrality (e.g. centrality = "median.weighted"). Also user-defined numeric values (e.g. from the central age model) can be used if this appears appropriate.
The proportion of the polar part and the cartesian part of the Abanico Plot can be modfied for display reasons (plot.ratio = 0.75). By default, the polar part spreads over 75 % and leaves 25 % for the part that shows the KDE graph.

The optional parameter layout allows to modify the entire plot more sophisticated. Each element of the plot can be addressed and its properties can be defined. This includes font type, size and decoration, colours and sizes of all plot items. To infer the definition of a specific layout style cf. get_Layout() or type eg. for the layout type "journal" get_Layout("journal"). A layout type can be modified by the user by assigning new values to the list object.

It is possible for the z-scale to specify where ticks are to be drawn by using the parameter at, e.g. at = seq(80, 200, 20), cf. function documentation of axis. Specifying tick positions manually overrides a zlim-definition.

Value

returns a plot object and, optionally, a list with plot calculus data.

Function version

0.1.2 (2015-03-04 14:53:26)

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
Inspired by a plot introduced by Galbraith & Green (1990)
R Luminescence Package Team

References

Galbraith, R. & Green, P., 1990. Estimating the component ages in a finite mixture. International Journal of Radiation Applications and Instrumentation. Part D. Nuclear Tracks and Radiation Measurements, 17 (3), pp. 197-206.

See Also

plot_RadialPlot, plot_KDE, plot_Histogram

Examples

```
## store original graphics parameters
par.old <- par(no.readonly = TRUE)

## load example data and recalculate to Gray
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <- Second2Gray(ExampleData.DeValues$BT998, c(0.0438,0.0019))

## plot the example data straightforward
plot_AbanicoPlot(data = ExampleData.DeValues)

## now with linear z-scale
plot_AbanicoPlot(data = ExampleData.DeValues,
                 log.z = FALSE)

## now with output of the plot parameters
plot1 <- plot_AbanicoPlot(data = ExampleData.DeValues,
                          output = TRUE)
str(plot1)
plot1$zlim

## now with adjusted z-scale limits
plot_AbanicoPlot(data = ExampleData.DeValues,
                 zlim = c(100, 200))

## now with adjusted x-scale limits
plot_AbanicoPlot(data = ExampleData.DeValues,
                 xlim = c(0, 60))

## now with rug to indicate individual values in KDE part
plot_AbanicoPlot(data = ExampleData.DeValues,
                 rug = TRUE)

## now with a smaller bandwidth for the KDE plot
plot_AbanicoPlot(data = ExampleData.DeValues,
```

```
                bw = 0.01)

## now with a histogram instead of the KDE plot
plot_AbanicoPlot(data = ExampleData.DeValues,
                hist = TRUE,
                kde = FALSE)

## now with a KDE plot and histogram with manual number of bins
plot_AbanicoPlot(data = ExampleData.DeValues,
                hist = TRUE,
                breaks = 20)

## now with a KDE plot and a dot plot
plot_AbanicoPlot(data = ExampleData.DeValues,
                dots = TRUE)

## now with user-defined plot ratio
plot_AbanicoPlot(data = ExampleData.DeValues,
                plot.ratio = 0.5)

## now with user-defined central value
plot_AbanicoPlot(data = ExampleData.DeValues,
                central.value = 120)

## now with weighted median as measure of centrality
plot_AbanicoPlot(data = ExampleData.DeValues,
                centrality = "median.weighted")

## now with median/quartile range as measure of centrality/dispersion
plot_AbanicoPlot(data = ExampleData.DeValues,
                centrality = "median",
                dispersion = "qr")

## now with user-defined green line for minimum age model
CAM <- calc_CentralDose(ExampleData.DeValues,
                        plot = FALSE)

plot_AbanicoPlot(data = ExampleData.DeValues,
                line = CAM,
                line.col = "darkgreen",
                line.label = "CAM")

## now create plot with legend, colour, different points and smaller scale
plot_AbanicoPlot(data = ExampleData.DeValues,
                legend = "Sample 1",
                col = "tomato4",
                bar.col = "peachpuff",
                pch = "R",
                cex = 0.8)

## now without 2-sigma bar, polygon, grid lines and central value line
plot_AbanicoPlot(data = ExampleData.DeValues,
                bar.col = "none",
                polygon.col = "none",
                grid.col = "none",
                y.axis = FALSE,
                lwd = 0)
```

```
## now with direct display of De errors, without 2-sigma bar
plot_AbanicoPlot(data = ExampleData.DeValues,
                 bar.col = "none",
                 ylab = "",
                 y.axis = FALSE,
                 error.bars = TRUE)

## now with user-defined axes labels
plot_AbanicoPlot(data = ExampleData.DeValues,
                 xlab = c("Data error [%]",
                          "Data precision",
                          "Kernel density"),
                 ylab = "Scatter",
                 zlab = "Equivalent dose [Gy]")

## now with minimum, maximum and median value indicated
plot_AbanicoPlot(data = ExampleData.DeValues,
                central.value = 150,
                stats = c("min", "max", "median"))

## now with a brief statistical summary
plot_AbanicoPlot(data = ExampleData.DeValues,
                summary = c("n", "in.ci"))

## now with another statistical summary as subheader
plot_AbanicoPlot(data = ExampleData.DeValues,
                summary = c("mean.weighted", "median"),
                summary.pos = "sub")

## now a plot with two 2-sigma bars for one data set
plot_AbanicoPlot(data = ExampleData.DeValues,
                 centrality = c(120, 160),
                 mtext = "n = 25")

## now the data set is split into sub-groups, one is manipulated
data.1 <- ExampleData.DeValues[1:15,]
data.2 <- ExampleData.DeValues[16:25,] * 1.3

## now a common dataset is created from the two subgroups
data.3 <- list(data.1, data.2)

## now the two data sets are plotted in one plot
plot_AbanicoPlot(data = data.3)

## now with some graphical modification
plot_AbanicoPlot(data = data.3,
                 col = c("steelblue4", "orange4"),
                 bar.col = c("steelblue3", "orange3"),
                 polygon.col = c("steelblue1", "orange1"),
                 pch = c(2, 6),
                 density = c(10, 20),
                 angle = c(30, 50),
                 summary = c("n", "in.ci"))

## create Abanico plot with predefined layout definition
plot_AbanicoPlot(data = ExampleData.DeValues,
```

```
                layout = "journal")

## now with predefined layout definition and further modifications
plot_AbanicoPlot(data = data.3,
                layout = "journal",
                col = c("steelblue4", "orange4"),
                bar.col = adjustcolor(c("steelblue3", "orange3"),
                                      alpha.f = 0.5),
                polygon.col = c("steelblue3", "orange3"))

## for further information on layout definitions see documentation
## of function get_Layout()

## restore original graphical parameters
par(par.old)
```

---

plot_DRTResults *Visualise dose recovery test results*

Description

The function provides a standardised plot output for dose recovery test measurements.

Usage

```
plot_DRTResults(values, given.dose, error.range = 10, preheat,
    boxplot = FALSE, mtext, summary, summary.pos, legend, legend.pos,
    par.local = TRUE, na.rm = FALSE, ...)
```

Arguments

values	RLum.Results or data.frame, (**required**): input values containing at least De and De error. To plot more than one data set in one figure, a list of the individual data sets must be provided (e.g. list(dataset.1, dataset.2)).
given.dose	numeric (optional): given dose used for the dose recovery test to normalise data. If only one given dose is provided this given dose is valid for all input data sets (i.e., values is a list). Otherwise a given dose for each input data set has to be provided (e.g., given.dose = c(100,200)). If no given.dose values are plotted without normalisation (might be useful for preheat plateau tests). Note: Unit has to be the same as from the input values (e.g., Seconds or Gray).
error.range	numeric: symmetric error range in percent will be shown as dashed lines in the plot. Set error.range to 0 to void plotting of error ranges.
preheat	numeric: optional vector of preheat temperatures to be used for grouping the De values. If specified, the temperatures are assigned to the x-axis.
boxplot	logical: optionally plot values, that are grouped by preheat temperature as boxplots. Only possible when preheat vector is specified.
mtext	character: additional text below the plot title.
summary	character (optional): adds numerical output to the plot. Can be one or more out of: "n" (number of samples), "mean" (mean De value), "mean.weighted" (error-weighted mean), "median" (median of the De values), "sdrel" (relative standard deviation in percent), "sdabs" (absolute standard deviation), "serel" (relative standard error) and "seabs" (absolute standard error).

summary.pos	numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the statistical summary. Alternatively, the keyword "sub" may be specified to place the summary below the plot header. However, this latter option in only possible if mtext is not used.
legend	character vector (optional): legend content to be added to the plot.
legend.pos	numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the legend to be plotted.
par.local	logical (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If par.local = FALSE, global parameters are inherited.
na.rm	logical: indicating wether NA values are removed before plotting from the input data set
...	further arguments and graphical parameters passed to plot.

Details

Procedure to test the accuracy of a measurement protocol to reliably determine the dose of a specific sample. Here, the natural signal is erased and a known laboratory dose administered which is treated as unknown. Then the De measurement is carried out and the degree of congruence between administered and recovered dose is a measure of the protocol's accuracy for this sample.
In the plot the normalised De is shown on the y-axis, i.e. obtained De/Given Dose.

Value

A plot is returned.

Function version

0.1.6 (2015-03-04 13:27:28)

Note

Further data and plot arguments can be added by using the appropiate R commands.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Michael Dietze, GFZ Potsdam (Germany),
R Luminescence Package Team

References

Wintle, A.G., Murray, A.S., 2006. A review of quartz optically stimulated luminescence characteristics and their relevance in single-aliquot regeneration dating protocols. Radiation Measurements, 41, 369-391.

See Also

plot

Examples

```
## read example data set and misapply them for this plot type
data(ExampleData.DeValues, envir = environment())

## plot values
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
given.dose = 2800, mtext = "Example data")

## plot values with legend
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
                given.dose = 2800,
                legend = "Test data set")

## create and plot two subsets with randomised values
x.1 <- ExampleData.DeValues$BT998[7:11,]
x.2 <- ExampleData.DeValues$BT998[7:11,] * c(runif(5, 0.9, 1.1), 1)

plot_DRTResults(values = list(x.1, x.2),
                given.dose = 2800)

## some more user-defined plot parameters
plot_DRTResults(values = list(x.1, x.2),
                given.dose = 2800,
                pch = c(2, 5),
                col = c("orange", "blue"),
                xlim = c(0, 8),
                ylim = c(0.85, 1.15),
                xlab = "Sample aliquot")

## plot the data with user-defined statistical measures as legend
plot_DRTResults(values = list(x.1, x.2),
                given.dose = 2800,
                summary = c("n", "mean.weighted", "sd"))

## plot the data with user-defined statistical measures as sub-header
plot_DRTResults(values = list(x.1, x.2),
                given.dose = 2800,
                summary = c("n", "mean.weighted", "sd"),
                summary.pos = "sub")

## plot the data grouped by preheat temperatures
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
                given.dose = 2800,
                preheat = c(200, 200, 200, 240, 240))
## read example data set and misapply them for this plot type
data(ExampleData.DeValues, envir = environment())

## plot values
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
                given.dose = 2800, mtext = "Example data")
## plot two data sets grouped by preheat temperatures
plot_DRTResults(values = list(x.1, x.2),
                given.dose = 2800,
                preheat = c(200, 200, 200, 240, 240))
```

```
## plot the data grouped by preheat temperatures as boxplots
plot_DRTResults(values = ExampleData.DeValues$BT998[7:11,],
                given.dose = 2800,
                preheat = c(200, 200, 200, 240, 240),
                boxplot = TRUE)
```

---

plot_GrowthCurve *Fit and plot a growth curve for luminescence data (Lx/Tx against dose)*

Description

A dose response curve is produced for luminescence measurements using a regenerative protocol.

Usage

```
plot_GrowthCurve(sample, na.rm = TRUE, fit.method = "EXP", fit.weights = TRUE,
    fit.includingRepeatedRegPoints = TRUE, fit.NumberRegPoints,
    fit.NumberRegPointsReal, fit.bounds = TRUE, NumberIterations.MC = 100,
   output.plot = TRUE, output.plotExtended = TRUE, output.plotExtended.single = FALSE,
    cex.global = 1, ...)
```

Arguments

sample	data.frame (**required**): data frame with three columns for x=Dose,y=LxTx,z=LxTx.Error, y1=TnTx. The column for the test dose response is optional, but requires 'TnTx' as column name if used.
na.rm	logical (with default): excludes NA values from the data set prior to any further operations.
fit.method	character (with default): function used for fitting. Possible options are: LIN, EXP, EXP OR LIN, EXP+LIN or EXP+EXP. See details.
fit.weights	logical (with default): option whether the fitting is done with or without weights. See details.
fit.includingRepeatedRegPoints	logical (with default): includes repeated points for fitting (TRUE/FALSE).
fit.NumberRegPoints	integer (optional): set number of regeneration points manually. By default the number of all (!) regeneration points is used automatically.
fit.NumberRegPointsReal	integer (optional): if the number of regeneration points is provided manually, the value of the real, regeneration points = all points (repeated points) including reg 0, has to be inserted.
fit.bounds	logical (with default): set lower fit bounds for all fitting parameters to 0. Limited for the use with the fit methods EXP, EXP+LIN and EXP OR LIN. Argument to be inserted for experimental application only!
NumberIterations.MC	integer (with default): number of Monte Carlo simulations for error estimation. See details.
output.plot	logical (with default): plot output (TRUE/FALSE).

`output.plotExtended`
: logical (with default): If TRUE, 3 plots on one plot area are provided: (1) growth curve, (2) histogram from Monte Carlo error simulation and (3) a test dose response plot. If FALSE, just the growth curve will be plotted. **Requires:** `output.plot = TRUE`.

`output.plotExtended.single`
: logical (with default): single plot output (TRUE/FALSE) to allow for plotting the results in single plot windows. Requires `output.plot = TRUE` and `output.plotExtended = TRUE`.

`cex.global`
: numeric (with default): global scaling factor.

`...`
: Further arguments and graphical parameters to be passed. Note: Standard arguments will only be passed to the growth curve plot. Supported: `xlim`, `ylim`, `main`, `xlab`, `ylab`

Details

Fitting methods

For all options (except for the LIN and the EXP OR LIN), the nls function with the port algorithm is used.
LIN: fits a linear function to the data using lm:

$$y = m * x + n$$

EXP: try to fit a function of the form

$$y = a * (1 - exp(-(x + c)/b))$$

Parameters b and c are approximated by a linear fit using lm. Note: b = D0

EXP OR LIN: works for some cases where an EXP fit fails. If the EXP fit fails, a LIN fit is done instead.
EXP+LIN: tries to fit an exponential plus linear function of the form:

$$y = a * (1 - exp(-(x + c)/b) + (g * x))$$

The De is calculated by iteration.
Note: In the context of luminescence dating, this function has no physical meaning. Therefore, no D0 value is returned.
EXP+EXP: tries to fit a double exponential function of the form

$$y = (a1 * (1 - exp(-(x)/b1))) + (a2 * (1 - exp(-(x)/b2)))$$

This fitting procedure is not robust against wrong start parameters and should be further improved.

Fit weighting

If the option `fit.weights = TRUE` is chosen, weights are calculated using provided signal errors (Lx/Tx error):

$$fit.weights = 1/error/(sum(1/error))$$

Error estimation using Monte Carlo simulation

Error estimation is done using a Monte Carlo (MC) simulation approach. A set of Lx/Tx values is constructed by randomly drawing curve data from samled from normal distributions. The normal distribution is defined by the input values (mean = value, sd = value.error). Then, a growth curve

fit is attempted for each dataset resulting in a new distribution of single De values. The sd of this distribution is becomes then the error of the De. With increasing iterations, the error value becomes more stable. **Note:** It may take some calculation time with increasing MC runs, especially for the composed functions (`EXP+LIN` and `EXP+EXP`).
Each error estimation is done with the function of the chosen fitting method.

Subtitle information
To avoid plotting the subtitle information, provide an empty user mtext `mtext = ""`. To plot any other subtitle text, use `mtext`.

Value

`RLum.Results` object containing the De (De, De Error, D01 value, D02 value, De.MC and Fit type) and the fit object nls object for `EXP`, `EXP+LIN` and `EXP+EXP`. In case of a resulting linear fit when using `EXP OR LIN`, a lm object is returned.
The formula `Formula` is returned as R expression for further evaluation. Additionally a plot is returned.

Function version

1.5 (2015-03-04 12:43:39)

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Michael Dietze, GFZ Potsdam (Germany),
R Luminescence Package Team

Examples

```
##(1) plot growth curve for a dummy data.set and show De value
data(ExampleData.LxTxData, envir = environment())
temp <- plot_GrowthCurve(LxTxData)
get_RLum.Results(temp)

##(1a) to access the fitting value try
get_RLum.Results(temp, data.object = "Fit")

##(2) plot the growth curve only - uncomment to use
##pdf(file = "~/Desktop/Growth_Curve_Dummy.pdf", paper = "special")
plot_GrowthCurve(LxTxData)
##dev.off()

##(3) plot growth curve with pdf output - uncomment to use, single output
##pdf(file = "~/Desktop/Growth_Curve_Dummy.pdf", paper = "special")
plot_GrowthCurve(LxTxData, output.plotExtended.single = TRUE)
##dev.off()
```

plot_Histogram *Plot a histogram with separate error plot*

Description

Function plots a predefined histogram with an accompanying error plot as suggested by Rex Galbraith at the UK LED in Oxford 2010.

Usage

```
plot_Histogram(data, na.exclude = TRUE, mtext, cex.global, breaks,
    se, rug, normal_curve, summary, summary.pos, colour, ...)
```

Arguments

data	data.frame or RLum.Results object (required): for data.frame: two columns: De (data[,1]) and De error (data[,2])
na.exclude	logical (with default): excludes NA values from the data set prior to any further operations.
mtext	character (optional): further sample information (mtext).
cex.global	numeric (with default): global scaling factor.
breaks	(with default): sets breakpoints for histogram. Works as in hist.
se	logical (optional): plots standard error points over the histogram, default is FALSE.
rug	logical (optional): adds rugs to the histogram, default is TRUE.
normal_curve	logical (with default): adds a normal curve to the histogram. Mean and sd are calculated from the input data. More see details section.
summary	character (optional): adds numerical output to the plot. Can be one or more out of: "n" (number of samples), "mean" (mean De value), "mean.weighted" (error-weighted mean), "median" (median of the De values), "kdemax" (maximum of the KDE), "sdrel" (relative standard deviation in percent), "sdabs" (absolute standard deviation), "serel" (relative standard error), "seabs" (absolute standard error), "skewness" (skewness) and "kurtosis" (kurtosis). Note: Keywords "kdemax" is implemented for consistency reasons, however, no KDE is shown. The bandwidth is calculated according to plot_KDE
summary.pos	numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the statistical summary. Alternatively, the keyword "sub" may be specified to place the summary below the plot header. However, this latter option in only possible if mtext is not used. In case of coordinate specification, y-coordinate refers to the right y-axis.
colour	numeric or character (with default): optional vector of length 4 which specifies the colours of the following plot items in exactly this order: histogram bars, rug lines, normal distribution curve and standard error points (e.g., c("grey", "black", "red", "grey")).
...	further arguments and graphical parameters passed to plot. If y-axis labels are provided, these must be specified as a vector of length 2 since the plot features two axes (e.g. ylab = c("axis label 1", "axis label 2")). Y-axes limits (ylim) must be provided as vector of length four, with the first two elements specifying the left axes limits and the latter two elements giving the right axis limits.

Details

If the normal curve is added, the y-axis in the histogram will show the probability density.

Function version

0.4.3 (2015-03-04 13:26:15)

Note

The input data is not restricted to a special type.

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

See Also

hist, plot

Examples

```
## load data
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <-
  Second2Gray(ExampleData.DeValues$BT998, dose.rate = c(0.0438,0.0019))

## plot histogram the easiest way
plot_Histogram(ExampleData.DeValues)

## plot histogram with some more modifications
plot_Histogram(ExampleData.DeValues,
               rug = TRUE,
               normal_curve = TRUE,
               cex.global = 0.9,
               pch = 2,
               colour = c("grey", "black", "blue", "green"),
               summary = c("n", "mean", "sdrel"),
               summary.pos = "topleft",
               main = "Histogram of De-values",
               mtext = "Example data set",
               ylab = c(expression(paste(D[e], " distribution")),
                        "Error"),
               xlim = c(100, 250),
               ylim = c(0, 0.1, 5, 20))
```

plot_KDE *Plot kernel density estimate with statistics*

Description

Plot a kernel density estimate of measurement values in combination with the actual values and associated error bars in ascending order. Optionally, statistical measures such as mean, median, standard deviation, standard error and quartile range can be provided visually and numerically.

Usage

```
plot_KDE(data, na.exclude = TRUE, weights = FALSE, values.cumulative = TRUE,
    centrality, dispersion, summary, summary.pos, polygon.col,
    order = TRUE, bw = "nrd0", output = FALSE, ...)
```

Arguments

data	data.frame or RLum.Results object (required): for data.frame: two columns: De (values[,1]) and De error (values[,2]). For plotting multiple data sets, these must be provided as list (e.g. list(dataset1, dataset2)).
na.exclude	logical (with default): exclude NA values from the data set prior to any further operations.
weights	logical (with default): calculate the KDE with De-errors as weights. Attention, using errors as weights will result in a plot similar to a a probability density plot, with all ambiguities related to this plot type!
values.cumulative	logical (with default): show cumulative individual data.
centrality	character: measure(s) of centrality, used for plotting vertical lines of the respective measure. Can be one out of "mean", "median", "mean.weighted", "median.weighted" and "kdemax".
dispersion	character: measure of dispersion, used for drawing the polygon that depicts the dose distribution. One out of "sd" (standard deviation),"2sd" (2 standard deviations) "qr" (quartile range).
summary	character (optional): adds numerical output to the plot. Can be one or more out of: "n" (number of samples), "mean" (mean De value), "mean.weighted" (error-weighted mean), "median" (median of the De values), "sdrel" (relative standard deviation in percent), "sdabs" (absolute standard deviation), "serel" (relative standard error), "seabs" (absolute standard error), "kdemax" (maximum of the KDE), "skewness" (skewness) and "kurtosis" (kurtosis).
summary.pos	numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the statistical summary. Alternatively, the keyword "sub" may be specified to place the summary below the plot header. However, this latter option in only possible if mtext is not used. In case of coordinate specification, y-coordinate refers to the right y-axis.
polygon.col	character or numeric (with default): colour of the polygon showing the dose dispersion around the central value. Only relevant if dispersion is specified.
order	logical: Order data in ascending order.
bw	character (with default): bin-width, chose a numeric value for manual setting.

output	logical: Optional output of numerical plot parameters. These can be useful to reproduce similar plots. Default is FALSE.
...	further arguments and graphical parameters passed to plot.

Details

The function allow passing several plot arguments, such as main, xlab, cex. However, as the figure is an overlay of two separate plots, ylim must be specified in the order: c(ymin_axis1, ymax_axis1, ymin_axis2, ymax_axis2) when using the cumulative values plot option. Similarly, if other than the default colours are desired, the argument col must be provided with colours in the following order: probability density function, De values, De error bars, sd or qr polygon. The line type (lty) for additional measures of centrality will cycle through the default values (1, 2, ...) by default, i.e. KDE line solid, further vertical lines dashed, dotted, dash-dotted and so on. To change this behaviour specify the desired order of line types (e.g. lty = c(1, 3, 2, 5)). See examples for some further explanations. For details on the calculation of the bin-width (parameter bw) see density.

Function version

3.5 (2015-03-04 13:25:51)

Note

The plot output is no 'PD' plot (cf. the discussion of Berger and Galbraith in Ancient TL; see references)!

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne,
R Luminescence Package Team

See Also

density, plot

Examples

```
## read example data set
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <-
  Second2Gray(ExampleData.DeValues$BT998, c(0.0438,0.0019))

## create plot straightforward
plot_KDE(data = ExampleData.DeValues)

## create plot with logarithmic x-axis
plot_KDE(data = ExampleData.DeValues,
         log = "x")

## create plot with user-defined labels and axes limits
plot_KDE(data = ExampleData.DeValues,
         main = "Dose distribution",
         xlab = "Dose [s]",
         ylab = c("KDE estimate", "Cumulative dose value"),
         xlim = c(100, 250),
```

```
         ylim = c(0, 0.08, 0, 30))

## create plot with centrality lines and distribution polygons
plot_KDE(data = ExampleData.DeValues,
         ylim = c(0, 0.08, 0, 35),
         centrality = c("median", "mean"),
         dispersion = "sd",
         polygon.col = "lightblue")

## create plot with statistical summary below header
plot_KDE(data = ExampleData.DeValues,
         summary = c("n", "median", "skewness", "qr"))

## create plot with statistical summary as legend
plot_KDE(data = ExampleData.DeValues,
         summary = c("n", "mean", "sdrel", "seabs"),
         summary.pos = "topleft")

## split data set into sub-groups, one is manipulated, and merge again
data.1 <- ExampleData.DeValues[1:15,]
data.2 <- ExampleData.DeValues[16:25,] * 1.3
data.3 <- list(data.1, data.2)

## create plot with two subsets straightforward
plot_KDE(data = data.3)

## create plot with two subsets and summary legend at user coordinates
plot_KDE(data = data.3,
         summary = c("n", "median", "skewness"),
         summary.pos = c(110, 0.07),
         col = c("blue", "orange"))

## example of how to use the numerical output of the function
## return plot output to draw a thicker KDE line
KDE <- plot_KDE(data = ExampleData.DeValues,
                output = TRUE)

## read out coordinates of KDE graph
KDE.x <- KDE$De.density[[1]]$x
KDE.y <- KDE$De.density[[1]]$y

## transform y-values to right y-axis dimensions
KDE.y <- KDE.y / max(KDE.y) * (nrow(ExampleData.DeValues) - 1) + 1

## draw the KDE line
lines(x = KDE.x,
      y = KDE.y,
      lwd = 3)
```

`plot_RadialPlot` *Function to create a Radial Plot*

Description

A Galbraith's radial plot is produced on a logarithmic or a linear scale.

Usage

```
plot_RadialPlot(data, na.exclude = TRUE, negatives = "remove",
    log.z = TRUE, central.value, centrality = "mean.weighted",
    mtext, summary, summary.pos, legend, legend.pos, stats, rug = FALSE,
    plot.ratio, bar.col, y.ticks = TRUE, grid.col, line, line.col,
    line.label, output = FALSE, ...)
```

Arguments

data	data.frame or RLum.Results object (required): for data.frame two columns: De (data[,1]) and De error (data[,2]). To plot several data sets in one plot, the data sets must be provided as list, e.g. list(data.1, data.2).
na.exclude	logical (with default): excludes NA values from the data set prior to any further operations.
negatives	character (with default): rule for negative values. Default is "remove" (i.e. negative values are removed from the data set).
log.z	logical (with default): Option to display the z-axis in logarithmic scale. Default is TRUE.
central.value	numeric: User-defined central value, primarily used for horizontal centering of the z-axis.
centrality	character or numeric (with default): measure of centrality, used for automatically centering the plot and drawing the central line. Can either be one out of "mean", "median", "mean.weighted" and "median.weighted" or a numeric value used for the standardisation.
mtext	character: additional text below the plot title.
summary	character (optional): adds numerical output to the plot. Can be one or more out of: "n" (number of samples), "mean" (mean De value), "mean.weighted" (error-weighted mean), "median" (median of the De values), "sdrel" (relative standard deviation in percent), "sdabs" (absolute standard deviation), "serel" (relative standard error), "seabs" (absolute standard error), "kdemax" (maximum of the KDE), "skewness" (skewness) and "kurtosis" (kurtosis) and "in.ci" (percent of samples in confidence interval, e.g. 2-sigma). Note: Keywords "kdemax", "skewness", "kurtosis" are implemented for consistency reasons, however, no KDE is shown. The bandwidth is calculated according to plot_KDE
summary.pos	numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the statistical summary. Alternatively, the keyword "sub" may be specified to place the summary below the plot header. However, this latter option is only possible if mtext is not used.
legend	character vector (optional): legend content to be added to the plot.
legend.pos	numeric or character (with default): optional position coordinates or keyword (e.g. "topright") for the legend to be plotted.
stats	character: additional labels of statistically important values in the plot. One or more out of the following: "min", "max", "median".
rug	logical: Option to add a rug to the z-scale, to indicate the location of individual values
plot.ratio	numeric: User-defined plot area ratio (i.e. curvature of the z-axis). If omitted, the default value (4.5/5.5) is used and modified automatically to optimise the z-axis curvature. The parameter should be decreased when data points are plotted outside the z-axis or when the z-axis gets too elliptic.

bar.col	character or numeric (with default): colour of the bar showing the 2-sigma range around the central value. To disable the bar, use "none". Default is "grey".
y.ticks	logical: Option to hide y-axis labels. Useful for data with small scatter.
grid.col	character or numeric (with default): colour of the grid lines (originating at [0,0] and stretching to the z-scale). To disable grid lines, use "none". Default is "grey".
line	numeric: numeric values of the additional lines to be added.
line.col	character or numeric: colour of the additional lines.
line.label	character: labels for the additional lines.
output	logical: Optional output of numerical plot parameters. These can be useful to reproduce similar plots. Default is FALSE.
...	Further plot arguments to pass. xlab must be a vector of length 2, specifying the upper and lower x-axes labels.

Details

Details and the theoretical background of the radial plot are given in the cited literature. This function is based on an S script of Rex Galbraith. To reduce the manual adjustments, the function has been rewritten. Thanks to Rex Galbraith for useful comments on this function.
Plotting can be disabled by adding the argument plot = "FALSE", e.g. to return only numeric plot output.

Earlier versions of the Radial Plot in this package had the 2-sigma-bar drawn onto the z-axis. However, this might have caused misunderstanding in that the 2-sigma range may also refer to the z-scale, which it does not! Rather it applies only to the x-y-coordinate system (standardised error vs. precision). A spread in doses or ages must be drawn as lines originating at zero precision (x0) and zero standardised estimate (y0). Such a range may be drawn by adding lines to the radial plot (line, line.col, line.label, cf. examples).

Value

Returns a plot object.

Function version

0.5.3 (2015-03-04 13:25:19)

Author(s)

Michael Dietze, GFZ Potsdam (Germany),
Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)
Based on a rewritten S script of Rex Galbraith, 2010
R Luminescence Package Team

References

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Galbraith, R.F., 2010. On plotting OSL equivalent doses. Ancient TL, 28 (1), 1-10.

Galbraith, R.F. & Roberts, R.G., 2012. Statistical aspects of equivalent dose and error calculation and display in OSL dating: An overview and some recommendations. Quaternary Geochronology, 11, 1-27.

See Also

plot, plot_KDE, plot_Histogram

Examples

```
## load example data
data(ExampleData.DeValues, envir = environment())
ExampleData.DeValues <- Second2Gray(ExampleData.DeValues$BT998, c(0.0438,0.0019))

## plot the example data straightforward
plot_RadialPlot(data = ExampleData.DeValues)

## now with linear z-scale
plot_RadialPlot(data = ExampleData.DeValues,
                log.z = FALSE)

## now with output of the plot parameters
plot1 <- plot_RadialPlot(data = ExampleData.DeValues,
                         log.z = FALSE,
                         output = TRUE)
plot1
plot1$zlim

## now with adjusted z-scale limits
plot_RadialPlot(data = ExampleData.DeValues,
                log.z = FALSE,
                zlim = c(100, 200))

## now the two plots with serious but seasonally changing fun
#plot_RadialPlot(data = data.3, fun = TRUE)

## now with user-defined central value, in log-scale again
plot_RadialPlot(data = ExampleData.DeValues,
                central.value = 150)

## now with a rug, indicating individual De values at the z-scale
plot_RadialPlot(data = ExampleData.DeValues,
                rug = TRUE)
```

```
## now with legend, colour, different points and smaller scale
plot_RadialPlot(data = ExampleData.DeValues,
                legend.text = "Sample 1",
                col = "tomato4",
                bar.col = "peachpuff",
                pch = "R",
                cex = 0.8)

## now without 2-sigma bar, y-axis, grid lines and central value line
plot_RadialPlot(data = ExampleData.DeValues,
                bar.col = "none",
                grid.col = "none",
                y.ticks = FALSE,
                lwd = 0)

## now with user-defined axes labels
plot_RadialPlot(data = ExampleData.DeValues,
                xlab = c("Data error [%]",
                         "Data precision"),
                ylab = "Scatter",
                zlab = "Equivalent dose [Gy]")

## now with minimum, maximum and median value indicated
plot_RadialPlot(data = ExampleData.DeValues,
                central.value = 150,
                stats = c("min", "max", "median"))

## now with a brief statistical summary
plot_RadialPlot(data = ExampleData.DeValues,
                summary = c("n", "in.ci"))

## now with another statistical summary as subheader
plot_RadialPlot(data = ExampleData.DeValues,
                summary = c("mean.weighted", "median"),
                summary.pos = "sub")

## now the data set is split into sub-groups, one is manipulated
data.1 <- ExampleData.DeValues[1:15,]
data.2 <- ExampleData.DeValues[16:25,] * 1.3

## now a common dataset is created from the two subgroups
data.3 <- list(data.1, data.2)

## now the two data sets are plotted in one plot
plot_RadialPlot(data = data.3)

## now with some graphical modification
plot_RadialPlot(data = data.3,
                col = c("darkblue", "darkgreen"),
                bar.col = c("lightblue", "lightgreen"),
                pch = c(2, 6),
                summary = c("n", "in.ci"),
                summary.pos = "sub",
                legend = c("Sample 1", "Sample 2"))
```

`plot_Risoe.BINfileData` *Plot single luminescence curves from a BIN file object*

Description

Plots single luminescence curves from an object returned by the readBIN2R function.

Usage

```
plot_Risoe.BINfileData(BINfileData, position, run, set, sorter = "POSITION",
    ltype = c("IRSL", "OSL", "TL", "RIR", "RBR", "RL"), curve.transformation,
    dose_rate, temp.lab, cex.global = 1, ...)
```

Arguments

`BINfileData`	Risoe.BINfileData-class (**required**): requires an S4 object returned by the readBIN2R function.
`position`	vector (optional): option to limit the plotted curves by position (e.g. `position = 1`, `position = c(1,3,5)`).
`run`	vector (optional): option to limit the plotted curves by run (e.g., `run = 1`, `run = c(1,3,5)`).
`set`	vector (optional): option to limit the plotted curves by set (e.g., `set = 1`, `set = c(1,3,5)`).
`sorter`	character (with default): the plot output can be ordered by "POSITION","SET" or "RUN". POSITION, SET and RUN are options defined in the Risoe Sequence Editor.
`ltype`	character (with default): option to limit the plotted curves by the type of luminescence stimulation. Allowed values: `"IRSL"`, `"OSL"`,`"TL"`, `"RIR"`, `"RBR"` (corresponds to LM-OSL), `"RL"`. All type of curves are plotted by default.
`curve.transformation`	character (optional): allows transforming CW-OSL and CW-IRSL curves to pseudo-LM curves via transformation functions. Allowed values are: `CW2pLM`, `CW2pLMi`, `CW2pHMi` and `CW2pPMi`. See details.
`dose_rate`	numeric (optional): dose rate of the irradition source at the measurement date. If set, the given irradiation dose will be shown in Gy. See details.
`temp.lab`	character (optional): option to allow for different temperature units. If no value is set deg. C is chosen.
`cex.global`	numeric (with default): global scaling factor.
`...`	further undocumented plot arguments.

Details

Nomenclature

See `Risoe.BINfileData-class`

curve.transformation

This argument allows transforming continuous wave (CW) curves to pseudo (linear) modulated curves. For the transformation, the functions of the package are used. Currently, it is not possible to pass further arguments to the transformation functions. The argument works only for `ltype` `OSL` and `IRSL`.

Irradiation time

Plotting the irradiation time (s) or the given dose (Gy) requires that the variable `IRR_TIME` has been set within the BIN-file. This is normally done by using the 'Run Info' option within the Sequence Editor or by editing in R.

Value

Returns a plot.

Function version

0.4.1 (2015-03-04 00:19:53)

Note

The function has been successfully tested for the Sequence Editor file output version 3 and 4.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Michael Dietze, GFZ Potsdam (Germany)
R Luminescence Package Team

References

Duller, G., 2007. Analyst. pp. 1-45.

See Also

`Risoe.BINfileData-class`,`readBIN2R`, `CW2pLM`, `CW2pLMi`, `CW2pPMi`, `CW2pHMi`

Examples

```
##load data
data(ExampleData.BINfileData, envir = environment())

##plot all curves from the first position to the desktop
#pdf(file = "~/Desktop/CurveOutput.pdf", paper = "a4", height = 11, onefile = TRUE)

##example - load from *.bin file
#BINfile<- file.choose()
#BINfileData<-readBIN2R(BINfile)

#par(mfrow = c(4,3), oma = c(0.5,1,0.5,1))
#plot_Risoe.BINfileData(CWOSL.SAR.Data,position = 1)
#mtext(side = 4, BINfile, outer = TRUE, col = "blue", cex = .7)
#dev.off()
```

plot_RLum *General plot function for RLum S4 class objects*

Description

Function calls object specific plot functions for RLum S4 class objects.

Usage

```
plot_RLum(object, ...)
```

Arguments

object	RLum (**required**): S4 object of class RLum
...	further arguments and graphical parameters that will be passed to the specific plot functions

Details

The function provides a generalised access point for plotting specific RLum objects.
Depending on the input object, the corresponding plot function will be selected. Allowed arguments can be found in the documentations of each plot function.

object		corresponding plot function
RLum.Data.Curve	:	plot_RLum.Data.Curve
RLum.Data.Spectrum	:	plot_RLum.Data.Spectrum
RLum.Data.Image	:	plot_RLum.Data.Image
RLum.Analysis	:	plot_RLum.Analysis
RLum.Results	:	plot_RLum.Results

Value

Returns a plot.

Function version

0.3 (2015-03-04 00:19:53)

Note

The provided plot output depends on the input object.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

#

See Also

plot_RLum.Data.Curve, RLum.Data.Curve, plot_RLum.Data.Spectrum, RLum.Data.Spectrum, plot_RLum.Data.Image, RLum.Data.Image, plot_RLum.Analysis, RLum.Analysis, plot_RLum.Results, RLum.Results

Examples

```
#load Example data
data(ExampleData.CW_OSL_Curve, envir = environment())

#transform data.frame to RLum.Data.Curve object
temp <- as(ExampleData.CW_OSL_Curve, "RLum.Data.Curve")

#plot RLum object
plot_RLum(temp)
```

---

plot_RLum.Analysis *Plot function for an RLum.Analysis S4 class object*

Description

The function provides a standardised plot output for curve data of an RLum.Analysis S4 class object

Usage

```
plot_RLum.Analysis(object, nrows = 3, ncols = 2, abline, combine = FALSE,
    curve.transformation, plot.single = FALSE, ...)
```

Arguments

object	RLum.Analysis (**required**): S4 object of class RLum.Analysis
nrows	integer (with default): sets number of rows for plot output
ncols	integer (with default): sets number of columns for plot output
abline	list (optional): allows to set similar ablines in each plot. This option uses the function do.call, meaning that every argument in the list has to be provided as list, e.g. abline = list(list(v = 120), list(v = 350)) produces two vertical ablines: One at 150 and another one at 350. Within the call all arguments supported by abline are fully supported,
combine	logical (with default): allows to combine all codeRLum.Data.Curve objects in one single plot. Works only for RLum.Analysis that comprises a single curve object (option is currently only roughly implemented),
curve.transformation	character (optional): allows transforming CW-OSL and CW-IRSL curves to pseudo-LM curves via transformation functions. Allowed values are: CW2pLM, CW2pLMi, CW2pHMi and CW2pPMi. See details.
plot.single	logical (with default): each curve is plotted in a single window, overwrites the settings of norws and ncols

... further arguments and graphical parameters will be passed to the plot function. Supported arguments: main, mtext, log, lwd, lty type, pch, col ... and for combine = TRUE also: xlim, ylim, xlab, ylab, sub, legend.text, legend.pos

Details

The function produces a multiple plot output. A file output is recommended (e.g., pdf).

curve.transformation

This argument allows transforming continuous wave (CW) curves to pseudo (linear) modulated curves. For the transformation, the functions of the package are used. Currently, it is not possible to pass further arguments to the transformation functions. The argument works only for ltype OSL and IRSL.

Please note: The curve transformation within this functions works roughly, i.e. every IRSL or OSL curve is transformed, without considerung whether it is measured with the PMT or not! However, for a fast look it might be helpful.

Value

Returns multiple plots.

Function version

0.2.0 (2015-03-04 19:15:10)

Note

Not all arguments available for plot will be passed! Only plotting of RLum.Data.Curve and RLum.Data.Spectrum objects are currently supported.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

#

See Also

plot, plot_RLum, plot_RLum.Data.Curve

Examples

```
###load data
data(ExampleData.BINfileData, envir = environment())

##convert values for position 1
temp <- Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos=1)
```

```
##plot all values
plot_RLum.Analysis(temp)

##plot (combine) TL curves in one plot
temp.sel <- get_RLum.Analysis(temp, recordType = "TL", keep.object = TRUE)
plot_RLum.Analysis(temp.sel, combine = TRUE, norm = TRUE, main = "TL combined")
```

---

plot_RLum.Data.Curve *Plot function for an RLum.Data.Curve S4 class object*

Description

The function provides a standardised plot output for curve data of an RLum.Data.Curve S4 class object

Usage

```
plot_RLum.Data.Curve(object, par.local = TRUE, norm = FALSE,
    ...)
```

Arguments

object	RLum.Data.Curve (**required**): S4 object of class RLum.Data.Curve
par.local	logical (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If par.local = FALSE, global parameters are inherited.
norm	logical (with default): allows curve normalisation to the highest count value
...	further arguments and graphical parameters that will be passed to the plot function

Details

Only single curve data can be plotted with this function. Arguments according to plot.

Value

Returns a plot.

Function version

0.1.5 (2015-03-04 00:19:53)

Note

Not all arguments of plot will be passed!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

#

See Also

plot, plot_RLum

Examples

```
##plot curve data

#load Example data
data(ExampleData.CW_OSL_Curve, envir = environment())

#transform data.frame to RLum.Data.Curve object
temp <- as(ExampleData.CW_OSL_Curve, "RLum.Data.Curve")

#plot RLum.Data.Curve object
plot_RLum.Data.Curve(temp)
```

---

plot_RLum.Data.Image *Plot function for an* RLum.Data.Image *S4 class object*

Description

The function provides a standardised plot output for image data of an RLum.Data.ImageS4 class object, mainly using the plot functions provided by the raster package.

Usage

```
plot_RLum.Data.Image(object, par.local = TRUE, plot.type = "plot.raster",
    ...)
```

Arguments

object	RLum.Data.Image (**required**): S4 object of class RLum.Data.Image
par.local	logical (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If par.local = FALSE global parameters are inherited.
plot.type	character (with default): plot types. Supported types are plot.raster, plotRGB or contour
...	further arguments and graphical parameters that will be passed to the specific plot functions.

Details

Details on the plot functions

Image is visualised as 2D plot usinng generic plot types provided by other packages.

Supported plot types:

`plot.type = "plot.raster"`

Uses the standard plot function for raster data from the package `raster`: `plot`. For each raster layer in a raster brick one plot is produced.

Arguments that are passed through the function call:

`main`,`axes`, `xlab`, `ylab`, `xlim`, `ylim`, `col`

`plot.type = "plotRGB"`

Uses the function `plotRGB` from the `raster` package. Only one image plot is produced as all layers in a brick a combined. This plot type is useful to see whether any signal is recorded by the camera. Arguments that are passed through the function call:

`main`,`axes`, `xlab`, `ylab`, `ext`, `interpolate`, `maxpixels`, `alpha`, `colNA`, `stretch`

`plot.type = "contour"`

Uses the function contour plot function from the `raster` function (`contour`). For each raster layer one contour plot is produced. Arguments that are passed through the function call:

`main`,`axes`, `xlab`, `ylab`, `xlim`, `ylim`, `col`

Value

Returns a plot.

Function version

0.1 (2015-03-04 00:19:53)

Note

This function has been created to faciliate the plotting of image data imported by the function `readSPE2R`. However, so far the function is not optimized to handle image data > ca. 200 MByte and thus plotting of such data is extremely slow.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

-

See Also

RLum.Data.Image, plot, plot_RLum, raster,

Examples

```
##load data
data(ExampleData.RLum.Data.Image, envir = environment())

##plot data
plot_RLum.Data.Image(ExampleData.RLum.Data.Image)
```

---

plot_RLum.Data.Spectrum

Plot function for an RLum.Data.Spectrum S4 class object

Description

The function provides a standardised plot output for spectrum data of an RLum.Data.Spectrum S4 class object

Usage

```
plot_RLum.Data.Spectrum(object, par.local = TRUE, plot.type = "contour",
    optical.wavelength.colours = TRUE, bg.channels, bin.rows = 1,
    bin.cols = 1, rug = TRUE, xaxis.energy = FALSE, legend.text,
    ...)
```

Arguments

object	RLum.Data.Spectrum (**required**): S4 object of class RLum.Data.Spectrum
par.local	logical (with default): use local graphical parameters for plotting, e.g. the plot is shown in one column and one row. If par.local = FALSE global parameters are inherited.
plot.type	character (with default): plot type, for 3D-plot use persp, or persp3d, for a 2D-plot contour, single or multiple.lines (along the time or temperature axis) or transect (along the wavelength axis) Note: The use of persp3d will produce a dynamic 3D surface plot on the screen.
optical.wavelength.colours	logical (with default): use optical wavelength colour palette. Note: For this, the spectrum range is limited: c(350,750). Own colours can be set with the argument col.
bg.channels	vector (optional): defines channel for background subtraction If a vector is provided the mean of the channels is used for subtraction. Note: Background subtraction is applied prior to channel binning
bin.rows	integer (with defaul): allow summing-up wavelength channels (horizontal binning), e.g. bin.rows = 2 two channels are summed up

bin.cols	integer (with default): allow summing-up channel counts (vertical binning) for plotting, e.g. bin.cols = 2 two channels are summed up
rug	logical (with default): enables or disables colour rug. Currently only implemented for plot type multiple.lines.
xaxis.energy	logical (with default): enables or disables energy instead of wavelength axis. Axis labelling are changed accordingly, so far no manual axis labelling is choosen.
legend.text	character (with default): possiblity to provide own legend text. This argument is only considered for plot types providing a legend, e.g. plot.type="transect"
...	further arguments and graphical parameters that will be passed to the plot function.

Details

Matrix structure

(cf. RLum.Data.Spectrum)

- rows (x-values): wavelengths/channels (xlim, xlab)
- columns (y-values): time/temperature (ylim, ylab)
- cells (z-values): count values (zlim, zlab)

Note: This nomenclature is valid for all plot types of this function!

Nomenclature for value limiting

xlim: Limits values along the wavelength axis
ylim: Limits values along the time/temperature axis
zlim: Limits values along the count value axis

Details on the plot functions

Spectrum is visualised as 3D or 2D plot. Both plot types are based on internal R plot functions.

plot.type = "persp"

Arguments that will be passed to persp:

- shade: default is 0.4
- phi: default is 30
- theta: default is 30
- expand: default is 1
- ticktype: default is detailed

Note: Further parameters can be adjusted via par. *For example to set the background transparent and reduce the thickness of the lines use:* par(bg = NA, lwd = 0.7) *previous the function call.*

plot.type = "single"
Per frame a single curve is returned. Frames are time or temperature steps.

plot.type = "multiple.lines"
All frames drawn in one frame.

`plot.type = "transect"`
Depending on the selected wavelength/channel range a transect over the time/temperature (y-axis) will be plotted along the wavelength/channels (x-axis). If the range contains more than one channel, values (z-values) are summed up. To select a transect use the `xlim` argument, e.g. `xlim = c(300,310)` plot along the summed up count values of channel 300 to 310.

Further arguments that will be passed (depending on the plot type)
`xlab`, `ylab`, `zlab`, `xlim`, `ylim`, `zlim`, `main`, `mtext`, `pch`, `type`, `border`, `box` `lwd`, `bty`

Value

Returns a plot.

Function version

0.3.5 (2015-03-21 10:14:55)

Note

Not all additional arguments (. . .) will be passed similarly!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

#

See Also

RLum.Data.Spectrum, plot, plot_RLum, persp, persp3d, contour

Examples

```
##load example data
data(ExampleData.XSYG, envir = environment())

##(1)plot simple spectrum (2D) - contour
plot_RLum.Data.Spectrum(TL.Spectrum,
                        plot.type="contour",
                        xlim = c(310,750),
                        ylim = c(0,300),
                        bin.rows=10,
                        bin.cols = 1)

##(2) plot simple spectrum (2D) - multiple.lines (with ylim)
plot_RLum.Data.Spectrum(TL.Spectrum,
                        plot.type="multiple.lines",
                        xlim = c(310,750),
                        ylim = c(0,100),
                        bin.rows=10,
                        bin.cols = 1)
```

```
##(3) plot 3d spectrum (uncomment for usage)
# plot_RLum.Data.Spectrum(TL.Spectrum, plot.type="persp",
# xlim = c(310,750), ylim = c(0,300), bin.rows=10,
# bin.cols = 1)
```

`plot_RLum.Results` *Plot function for an RLum.Results S4 class object*

Description

The function provides a standardised plot output for data of an RLum.Results S4 class object

Usage

```
plot_RLum.Results(data, single = TRUE, ...)
```

Arguments

`data`	`RLum.Results` (**required**): S4 object of class `RLum.Results`
`single`	`logical` (with default): single plot output (`TRUE/FALSE`) to allow for plotting the results in as few plot windows as possible.
`...`	further arguments and graphical parameters will be passed to the `plot` function.

Details

The function produces a multiple plot output. A file output is recommended (e.g., `pdf`).

Value

Returns multiple plots.

Function version

0.1 (2015-03-10 09:43:59)

Note

Not all arguments available for `plot` will be passed! Only plotting of `RLum.Results` objects are supported.

Author(s)

Christoph Burow, University of Cologne (Germany)
R Luminescence Package Team

References

#

See Also

plot, plot_RLum,

Examples

```
###load data
data(ExampleData.DeValues, envir = environment())

# apply the un-logged minimum age model
mam<- calc_MinDose(data = ExampleData.DeValues$CA1, sigmab = 0.2, log = TRUE, plot = FALSE)

##plot
plot_RLum.Results(mam)

# estimate the number of grains on an aliquot
grains<- calc_AliquotSize(grain.size = c(100,150), sample.diameter = 1, plot = FALSE)

##plot
plot_RLum.Results(grains)
```

---

readBIN2R *Import Risoe BIN-file into R*

Description

Import a *.bin or a *.binx file produced by a Risoe DA15 and DA20 TL/OSL reader into R.

Usage

```
readBIN2R(file, show.raw.values = FALSE, n.records, show.record.number = FALSE,
    txtProgressBar = TRUE, forced.VersionNumber)
```

Arguments

file	character (**required**): bin-file name (including path), e.g. [WIN]: `readBIN2R("C:/Desktop/test.bin")`, [MAC/LINUX]: `readBIN2R("/User/test/Desktop/test.bin")`
show.raw.values	logical (with default): shows raw values from BIN file for `LTYPE`, `DTYPE` and `LIGHTSOURCE` without translation in characters.
n.records	raw (optional): limits the number of imported records. Can be used in combination with `show.record.number` for debugging purposes, e.g. corrupt BIN files.
show.record.number	logical (with default): shows record number of the imported record, for debugging usage only.
txtProgressBar	logical (with default): enables or disables `txtProgressBar`.

`forced.VersionNumber`
: integer (optional): allows to cheat the version number check in the function by own values for cases where the BIN-file version is not supported.
Note: The usage is at own risk, only supported BIN-file versions have been tested.

Details

The binary data file is parsed byte by byte following the data structure published in the Appendices of the Analyst manual p. 42.

For the general BIN-file structure, the reader is referred to the Risoe website: `http://www.nutech.dtu.dk/`

Value

Returns an S4 Risoe.BINfileData-class object containing two slots:

`METADATA`
: A data.frame containing all variables stored in the bin-file.

`DATA`
: A list containing a numeric vector of the measured data. The ID corresponds to the record ID in METADATA.

Function version

0.8.1 (2015-03-04 12:43:39)

Note

The function has been successfully tested for BIN format versions 03, 04 and 06. The version number depends on the used Sequence Editor.

Other BIN format versions are currently not supported.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), Margret C. Fuchs, AWI Potsdam (Germany),
R Luminescence Package Team

References

Duller, G., 2007. Analyst. http://www.nutech.dtu.dk/english/~/media/Andre_Universitetsenheder/Nutech/Produkter%20og%20services/Dosimetri/radiation_measurement_instruments/tl_osl_reader/Manuals/analyst_manual_v3_22b.ashx

See Also

`writeR2BIN`, `Risoe.BINfileData`, `readBin`, `merge_Risoe.BINfileData`, `txtProgressBar`

Examples

```
##(1) import Risoe BIN-file to R (uncomment for usage)

#FILE <- file.choose()
#temp <- readBIN2R(FILE)
#temp
```

---

readSPE2R *Import Princeton Intruments (TM) SPE-file into R*

Description

Function imports Princeton Instruments (TM) SPE-files into R environment and provides RLum objects as output.

Usage

```
readSPE2R(file, output.object = "RLum.Data.Image", frame.range,
    txtProgressBar = TRUE)
```

Arguments

file	character (**required**): spe-file name (including path), e.g. [WIN]: readSPE2R("C:/Desktop/test.spe"), [MAC/LINUX]: readSPER("/User/test/Desktop/test.spe")
output.object	character (with default): set RLum output object. Allowed types are "RLum.Data.Spectrum", "RLum.Data.Image" or "matrix"
frame.range	vector (optional): limit frame range, e.g. select first 100 frames by frame.range = c(1,100)
txtProgressBar	logical (with default): enables or disables txtProgressBar.

Details

Function provides an import routine for the Princton Instruments SPE format. Import functionality is based on the file format description provided by Princton Instruments and a MatLab script written by Carl Hall (s. references).

Value

Depending on the chosen option the functions returns three different type of objects:

output.object.

RLum.Data.Spectrum

An object of type RLum.Data.Spectrum is returned. Row sums are used to integrate all counts over one channel.

RLum.Data.Image

An object of type RLum.Data.Image is returned. Due to performace reasons the import is aborted for files containing more than 100 frames. This limitation can be overwritten manually by using the argument frame.frange.

matrix

Returns a matrix of the form: Rows = Channels, columns = Frames For the transformation the function get_RLum.Data.Spectrum is used, meaning that the same results can be obtained by using the function get_RLum.Data.Spectrum on an RLum.Data.Spectrum object or get_RLum.Data.Image on an RLum.Data.Image object.

Function version

0.1 (2015-03-04 12:43:39)

Note

The function does not test whether the input data are spectra or pictures for spatial resolved analysis!

The function has been successfully tested for SPE format versions 2.x.

Currently not all information provided by the SPE format are supported.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France), R Luminescence Package Team

References

Princeton Instruments, 2014. Princeton Instruments SPE 3.0 File Format Specification, Version 1.A, ftp://ftp.princetoninstruments.com/Public/Manuals/Princeton%20Instruments/SPE%203.0%20File%20Format%20Specification.pdf

Hall, C., 2012: readSPE.m. http://www.mathworks.com/matlabcentral/fileexchange/35940-readspe/content/readSPE.m

See Also

readBin, RLum.Data.Spectrum, raster

Examples

```
## to run examples uncomment lines and run the code

##(1) Import data as RLum.Data.Spectrum object
#file <- file.choose()
#temp <- readSPE2R(file)
#temp

##(2) Import data as RLum.Data.Image object
#file <- file.choose()
#temp <- readSPE2R(file, output.object = "RLum.Data.Image")
#temp
```

```
##(3) Import data as matrix object
#file <- file.choose()
#temp <- readSPE2R(file, output.object = "matrix")
#temp

##(4) Export raw data to csv, if temp is a RLum.Data.Spectrum object
# write.table(x = get_RLum.Data.Spectrum(temp),
#             file = "[your path and filename]",
#             sep = ";", row.names = FALSE)
```

`readXSYG2R` *Import XSYG files to R*

Description

Imports XSYG files produced by a Freiberg Instrument lexsyg reader into R.

Usage

```
readXSYG2R(file, recalculate.TL.curves = TRUE, import = TRUE,
    txtProgressBar = TRUE)
```

Arguments

`file`	character (**required**): path and file name of the XSYG file.
`recalculate.TL.curves`	logical (with default): if set to `TRUE`, TL curves are returned as temperature against count values (see details for more information) Note: The option overwrites the time vs. count TL curve. Select `FALSE` to import the raw data delivered by the lexsyg. Works for TL curves and spectra.
`import`	logical (with default): if set to `FALSE`, only the XSYG file structure is shown.
`txtProgressBar`	logical (with default): enables `TRUE` or disables `FALSE` the progression bar during import

Details

How does the import function work?

The function uses the `xml` package to parse the file structure. Each sequence is subsequently translated into an `RLum.Analysis` object.

General structure XSYG format

```
<?xml?
<Sample>
<Sequence>
<Record>
```

```
<Curve name="first curve" />
<Curve name="curve with data">
x0 , y0 ; x1 , y1 ; x2 , y2 ; x3 , y3
</Curve>
</Record>
</Sequence>
</Sample>
```

So far, each XSYG file can only contain one `<Sample></Sample>`, but multiple sequences.

Each record may comprise several curves.

TL curve recalculation

On the FI lexsyg device TL curves are recorded as time against count values. Temperature values are monitored on the heating plate and stored in a separate curve (time vs. temperature). If the option `recalculate.TL.curves = TRUE` is chosen, the time values for each TL curve are replaced by temperature values.

Practically, this means combining two matrices (Time vs. Counts and Time vs. Temperature) with different row numbers by their time values. Three cases are considered:

HE: Heating element
PMT: Photomultiplier tube
Interpolation is done using the function `approx`

CASE (1): `nrow(matrix(PMT)) > nrow(matrix(HE))`

Missing temperature values from the heating element are calculated using time values from the PMT measurement.

CASE (2): `nrow(matrix(PMT)) < nrow(matrix(HE))`

Missing count values from the PMT are calculated using time values from the heating element measurement.

CASE (3): `nrow(matrix(PMT)) == nrow(matrix(HE))`

A new matrix is produced using temperature values from the heating element and count values from the PMT.

Note: Please note that due to the recalculation of the temperature values based on values delivered by the heating element, it may happen that mutiple count values exists for each temperature value and temperature values may also decrease during heating, not only increase.

Value

Using the option `import = FALSE`

A list consisting of two elements is shown:

`Sample` data.frame with information on file.

`Sequences` data.frame with information on the sequences stored in the XSYG file

.

Using the option `import = TRUE` (default)

A list is provided, the list elements contain:

`Sequence.Header`
data.frame with information on the sequence.

`Sequence.Object`
`RLum.Analysis` containing the curves.

Function version

0.4.1 (2015-03-21 03:09:47)

Note

This function is a beta version as the XSYG file format is not yet fully specified. Thus, further file operations (merge, export, write) should be done using the functions provided with the package `xml`.

So far, no image data import is provided!
Corresponding values in the XSXG file are skipped.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

Grehl, S., Kreutzer, S., Hoehne, M., 2013. Documentation of the XSYG file format. Unpublished Technical Note. Freiberg, Germany

Further reading

XML: http://en.wikipedia.org/wiki/XML

See Also

`xml`, `RLum.Analysis`, `RLum.Data.Curve`, `approx`

Examples

```
##(1) import XSYG file to R (uncomment for usage)

#FILE <- file.choose()
#temp <- readXSYG2R(FILE)

##(2) additional examples for pure XML import using the package XML
##    (uncomment for usage)
```

```
  ##import entire XML file
  #FILE <- file.choose()
  #temp <- xmlRoot(xmlTreeParse(FILE))

  ##search for specific subnodes with curves containing 'OSL'
  #getNodeSet(temp, "//Sample/Sequence/Record[@recordType = 'OSL']/Curve")

##(2) How to extract single curves ... after import
data(ExampleData.XSYG, envir = environment())

##grep one OSL curves and plot the first curve
OSLcurve <- get_RLum.Analysis(OSL.SARMeasurement$Sequence.Object, recordType="OSL")[[1]]

##(3) How to see the structure of an object?
get_structure.RLum.Analysis(OSL.SARMeasurement$Sequence.Object)
```

Risoe.BINfileData-class

Class "Risoe.BINfileData"

Description

S4 class object for luminescence data in R. The object is produced as output of the function readBIN2R.

Objects from the Class

Objects can be created by calls of the form new("Risoe.BINfileData", ...).

Slots

METADATA: Object of class "data.frame" containing the meta information for each curve.

DATA: Object of class "list" containing numeric vector with count data.

.RESERVED: Object of class "list" containing list of undocumented raw values for internal use only.

.S3Class: Object of class "character"

Methods

show signature(object = "Risoe.BINfileData"): ...

set_Risoe.BINfileData signature(METADATA = "data.frame", DATA = "list", .RESERVED = "list"):
The Risoe.BINfileData is normally produced as output of the function readBIN2R. This construction method is intended for internal usage only.

get_Risoe.BINfileData signature(object = "Risoe.BINfileData"):
Formal get-method for Risoe.BINfileData object. It does not allow accessing the object directly, it is just showing a terminal message.

Version

0.4 (2014-02-27)

Note

Internal METADATA - object structure

#	Name	Data Type	V	Description
[,1]	ID	numeric	RLum	Unique record ID (same ID as in slot DATA)
[,2]	SEL	logic	RLum	Record selection, not part official BIN-format, triggered by TAG
[,3]	VERSION	raw	03-06	BIN-file version number
[,4]	LENGTH	integer	03-06	Length of this record
[,5]	PREVIOUS	integer	03-06	Length of previous record
[,6]	NPOINTS	integer	03-06	Number of data points in the record
[,7]	RUN	integer	03-06	Run number
[,8]	SET	integer	03-06	Set number
[,9]	POSITION	integer	03-06	Position number
[,10]	GRAIN	integer	03-04	Grain number
[,11]	GRAINNUMBER	integer	06	Grain number
[,12]	CURVENO	integer	06	Curve number
[,13]	XCOORD	integer	03-06	X position of a single grain
[,14]	YCOORD	integer	03-06	Y position of a single grain
[,15]	SAMPLE	factor	03-06	Sample name
[,16]	COMMENT	factor	03-06	Comment name
[,17]	SYSTEMID	integer	03-06	Risoe system id
[,18]	FNAME	factor	06	File name (*.bin/*.binx)
[,19]	USER	facotr	03-06	User name
[,20]	TIME	character	03-06	Data collection time (hh-mm-ss)
[,21]	DATE	factor	03-06	Data collection date (ddmmyy)
[,22]	DTYPE	character	03-06	Data type
[,23]	BL_TIME	numeric	03-06	Bleaching time
[,24]	BL_UNIT	integer	03-06	Bleaching unit (mJ, J, secs, mins, hrs)
[,25]	NORM1	numeric	03-06	Normalisation factor (1)
[,26]	NORM2	numeric	03-06	Normalisation factor (2)
[,27]	NORM3	numeric	03-06	Normalisation factor (3)
[,28]	BG	numeric	03-06	Background level
[,29]	SHIFT	integer	03-06	Number of channels to shift data
[,30]	TAG	integer	03-06	Tag, triggers SEL
[,31]	LTYPE	character	03-06	Luminescence type
[,32]	LIGHTSOURCE	character	03-06	Light source
[,33]	LPOWER	numeric	03-06	Optical stimulation power
[,34]	LIGHTPOWER	numeric	06	Optical stimulation power
[,35]	LOW	numeric	03-06	Low (temperature, time, wavelength)
[,36]	HIGH	numeric	03-06	High (temperature, time, wavelength)
[,37]	RATE	numeric	03-06	Rate (heating rate, scan rate)
[,38]	TEMPERATURE	integer	03-06	Sample temperature
[,39]	MEASTEMP	integer	06	Measured temperature
[,40]	AN_TEMP	numeric	03-06	Annealing temperature
[,41]	AN_TIME	numeric	03-06	Annealing time
[,42]	TOLDELAY	integer	03-06	TOL 'delay' channels
[,43]	TOLON	integer	03-06	TOL 'on' channels
[,44]	TOLOFF	integer	03-06	TOL 'off' channels

[,45]	IRR_TIME	numeric	03-06	Irradiation time
[,46]	IRR_TYPE	integer	03-06	Irradiation type (alpha, beta or gamma)
[,47]	IRR_UNIT	integer	03-04	Irradiation unit (Gy, Rads, secs, mins, hrs)
[,48]	IRR_DOSERATE	numeric	06	Irradiation dose rate (Gy/s)
[,49]	IRR_DOSERATEERR	numeric	06	Irradiation dose rate error (Gy/s)
[,50]	TIMESINCEIRR	integer	06	Time since irradiation (s)
[,51]	TIMETICK	numeric	06	Time tick for pulsing (s)
[,52]	ONTIME	integer	06	On-time for pulsing (in time ticks)
[,53]	STIMPERIOD	integer	06	Stimulation period (on+off in time ticks)
[,54]	GATE_ENABLED	raw	06	PMT signal gating enabled
[,55]	ENABLE_FLAGS	raw	03	PMT signal gating enabled
[,56]	GATE_START	integer	06	Start gating (in time ticks)
[,57]	GATE_STOP	ingeter	06	Stop gating (in time ticks), 'Gateend' for version 04, here only G
[,58]	PTENABLED	raw	06	Photon time enabled
[,59]	DTENABLED	raw	06	PMT dead time correction enabled
[,60]	DEADTIME	numeric	06	PMT dead time (s)
[,61]	MAXLPOWER	numeric	06	Stimulation power to 100 percent (mW/cm^2)
[,62]	XRF_ACQTIME	numeric	06	XRF acquisition time (s)
[,63]	XRF_HV	numeric	06	XRF X-ray high voltage (V)
[,64]	XRF_CURR	integer	06	XRF X-ray current (uA)
[,65]	XRF_DEADTIMEF	numeric	06	XRF dead time fraction
[,66]	SEQUENCE	character	03-04	Sequence name

V = BIN-file version (RLum means that it does not depend on a specific BIN version)

Note that the `Risoe.BINfileData` object combines all values from different versions from the BIN-file, reserved bits are skipped, however, the function `writeR2BIN` reset arbitrary reserved bits. Invalid values for a specific version are set to `NA`. Furthermore, the internal R data types do not necessarily match the required data types for the BIN-file data import! Data types are converted during data import.

LTYPES

[,0]	TL	: Thermoluminescence
[,1]	OSL	: Optically stimulated luminescence
[,2]	IRSL	: Infrared stimulated luminescence
[,3]	M-IR	: Infrared monochromator scan
[,4]	M-VIS	: Visible monochromator scan
[,5]	TOL	: Thermo-optical luminescence
[,6]	TRPOSL	: Time Resolved Pulsed OSL
[,7]	RIR	: Ramped IRSL
[,8]	RBR	: Ramped (Blue) LEDs
[,9]	USER	: User defined
[,10]	POSL	: Pulsed OSL
[,11]	SGOSL	: Single Grain OSL
[,12]	RL	: Radio Luminescence
[,13]	XRF	: X-ray Fluorescence

LTYPES

[,0]	0	Natural

[,1]	1	N+dose
[,2]	2	Bleach
[,3]	3	Bleach+dose
[,4]	4	Natural (Bleach)
[,5]	5	N+dose (Bleach)
[,6]	6	Dose
[,7]	7	Background

(information on the LTYPE and DTYPE kindly provided by Risoe, DTU Nutech)

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

References

Risoe DTU, 2013. The Sequence Editor User Manual - Feb 2013

http://www.nutech.dtu.dk/

See Also

plot_Risoe.BINfileData, readBIN2R, writeR2BIN,merge_Risoe.BINfileData, Risoe.BINfileData2RLum.Analys
Risoe.BINfileData2RLum.Data.Curve

Examples

```
showClass("Risoe.BINfileData")
```

Risoe.BINfileData2RLum.Analysis

Convert Risoe.BINfileData object to an RLum.Analysis object

Description

Converts values from one specific position of a Risoe.BINfileData S4-class object to an RLum.Analysis object.

Usage

```
Risoe.BINfileData2RLum.Analysis(object, pos, run, set, ltype,
    protocol = "unknown")
```

Arguments

object	Risoe.BINfileData (**required**): Risoe.BINfileData object
pos	integer (**required**): position number of the Risoe.BINfileData object for which the curves are stored in the RLum.Analysis object. If the position is not valid NA is returned.
run	vector, numeric (optional): run number from the measurement to limit the converted data set (e.g., run = c(1:48)).

`set`	`vector`, `numeric` (optional): set number from the measurement to limit the converted data set (e.g., `set = c(1:48)`).
`ltype`	`vector`, `character` (optional): curve type to limit the converted data. Allowed values are: `IRSL`, `OSL`, `TL`, `RIR`, `RBR` and `USER`
`protocol`	`character` (optional): sets protocol type for analysis object. Value may be used by subsequent analysis functions.

Details

The `RLum.Analysis` object requires a set of curves for specific further protocol analyses. However, the `Risoe.BINfileData` usually contains a set of curves for different aliquots and different protocol types that may be mixed up. Therefore, a conversion is needed.

Value

Returns an `RLum.Analysis` object.

Function version

0.1.2 (2015-03-04 00:19:53)

Note

The `protocol` argument of the `RLum.Analysis` object is set to 'unknown' if not stated otherwise.

Author(s)

Sebastian Kreutzer, JLU Giessen (Germany),
R Luminescence Package Team

References

#

See Also

`Risoe.BINfileData`, `RLum.Analysis`, `readBIN2R`

Examples

```
##load data
data(ExampleData.BINfileData, envir = environment())

##convert values for position 1
Risoe.BINfileData2RLum.Analysis(CWOSL.SAR.Data, pos = 1)
```

Risoe.BINfileData2RLum.Data.Curve *Convert an element from a Risoe.BINfileData object to an RLum.Data.Curve object*

Description

The function converts one specified single record from a Risoe.BINfileData object to an RLum.Data.Curve object.

Usage

```
Risoe.BINfileData2RLum.Data.Curve(object, id, pos, run, set)
```

Arguments

object	Risoe.BINfileData (**required**): Risoe.BINfileData object
id	integer (**required**): record id in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If no value for id is provided, the record has to be specified by pos, set and run.
pos	integer (optional): record position number in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If a value for id is provided, this argument is ignored.
run	integer (optional): record run number in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If a value for id is provided, this argument is ignored.
set	integer (optional): record set number in the Risoe.BINfileData object of the curve that is to be stored in the RLum.Data.Curve object. If a value for id is provided, this argument is ignored.

Details

The function extracts all METADATA from the Risoe.BINfileData object and stores them in the RLum.Data.Curve object.

Value

Returns an RLum.Data.Curve object.

Function version

0.1 (2015-03-04 00:19:53)

Note

The function is intended for experimental usage. Normally, the function Risoe.BINfileData2RLum.Analysis should be used for the conversion.

Author(s)

Sebastian Kreutzer, Freiberg Instruments/JLU Giessen (Germany),
R Luminescence Package Team

References

#

See Also

Risoe.BINfileData2RLum.Analysis, set_RLum.Data.Curve, RLum.Data.Curve, RLum.Analysis, Risoe.BINfileData, plot_RLum

Examples

```
##get package example data
data(ExampleData.BINfileData, envir = environment())

##convert one record
Risoe.BINfileData2RLum.Data.Curve(CWOSL.SAR.Data, id = 1)
```

RLum-class *Class* "RLum"

Description

Abstract class for data in the package Luminescence

Objects from the Class

A virtual Class: No objects can be created from it.

Slots

`.S3Class`**:** Object of class `"character"`

Methods

No methods defined with class "RLum" in the signature.

Version

0.1 (2013-01-18)

Note

RLum is a virtual class.

Author(s)

Sebastian Kreutzer, 2013 (Freiberg Instruments/JLU Giessen, Germany)

References

#

See Also

RLum.Data, RLum.Analysis

Examples

```
showClass("RLum")
```

RLum.Analysis-class *Class* "RLum.Analysis"

Description

Object class containing analysis data for protocol analysis.

Objects from the Class

Objects can be created by calls of the form `new("RLum.Analysis", ...)`.

Slots

`records`**:** Object of class `"list"` containing objects of class RLum.Data

`protocol`**:** Object of class `"character"` describing the applied measurement protocol

`.S3Class`**:** Object of class `"character"`

Methods

show `signature(object = "RLum.Analysis")`: ...

set_RLum.Analysis `signature(records = "list", protocol = "character")`:

Construction method for `RLum.Analysis` object. The slot `protocol` is optional and predefined as `UNKNOWN` by default.

get_RLum.Analysis `signature(object = "RLum.Analysis",` r

Accessor method for `RLum.Analysis` object.

The slots `record.id`, `recordType`, `curveType` and `RLum.type` are optional to allow for records limited by their id (list index number), their record type (e.g. `recordType = "OSL"`) or object type.

Example: curve type (e.g. `curveType = "predefined"` or `curveType ="measured"`)

The selection of a specific `RLum.type` **object superimposes the default selection.** Currently supported objects are: `RLum.Data.Curve` and `RLum.Data.Spectrum`

The argument `get.index = TRUE` just returns a numeric vector with the index of each element in the `RLum.Analysis` object.

The argument `keep.object` allowing returns an `RLum.Analysis` object instead of the single elements. Default is `keep.object = FALSE`.

get_structure.RLum.Analysis `signature(object = "RLum.Analysis")`: get meta structure of object as `data.frame`

length_RLum.Analysis `signature(object = "RLum.Analysis")`: returns length of the object, i.e., number of records in the object

Version

0.1.4 (2014-02-26)

Note

The method `get_structure.RLum.Analysis` is currently just avaiblable for objects containing `RLum.Data.Curve`.

Author(s)

Sebastian Kreutzer, Freiberg Instruments/JLU Giessen (Germany)

References

#

See Also

`Risoe.BINfileData2RLum.Analysis`, `Risoe.BINfileData`, `RLum`

Examples

```
showClass("RLum.Analysis")

## usage of get_RLum.Analysis() with returining an RLum.Analysis object
#  get_RLum.Analysis(object, keep.object = TRUE)
```

RLum.Data-class *Class* "RLum.Data"

Description

Generalized virtual data class for luminescence data.

Objects from the Class

A virtual Class: No objects can be created from it.

Slots

`.S3Class`**:** Object of class `"character"`

Methods

No methods defined with class "RLum.Data" in the signature.

Version

0.1 (2013-01-18)

Note

Just a virtual class.

Author(s)

Sebastian Kreutzer, 2013 (Freiberg Instruments/JLU Giessen, Germany)

References

#

See Also

RLum, RLum.Data.Curve, RLum.Data.Spectrum

Examples

```
showClass("RLum.Data")
```

RLum.Data.Curve-class *Class* "RLum.Data.Curve"

Description

Class for luminescence curve data.

Objects from the Class

Objects can be created by calls of the form `new("RLum.Data.Curve", ...)`.

Slots

recordType: Object of class "character" containing the type of the curve (e.g. "TL" or "OSL")

curveType: Object of class "character" containing curve type, allowed values are `measured` or `predefined`

data: Object of class "matrix" containing curve x and y data

info: Object of class "list" containing further meta information objects

.S3Class: Object of class "character"

Extends

Class "RLum.Data".

Methods

coerce `signature(from = "data.frame", to = "RLum.Data.Curve")`
`signature(from = "matrix", to = "RLum.Data.Curve")`
Furthermore, lossy coercing is possible from `RLum.Data.Curve` to:

`data.frame`, `matrix`

show `signature(object = "RLum.Data.Curve")`: ...

set_RLum.Data.Curve `signature(recordType = "character", curveType = "character", data = "matrix",`
Construction method for `RLum.Data.Curve` object. The slot `info` is optional and predefined as empty `list` by default.

get_RLum.Data.Curve `signature(object = "RLum.Data.Curve", info.object = "character")`:
Accessor method for `RLum.Data.Curve` object. The argument `info.object` is optional to directly access the info elements. If no info element name is provided, the raw curve data (`matrix`) will be returned.

Version

0.1.2 (2013-11-22)

Note

The class should only contain data for a single curve. For additional elements the slot `info` can be used (e.g. providing additional heating ramp curve).

Author(s)

Sebastian Kreutzer Freiberg Instruments/JLU Giessen (Germany)

References

#

See Also

`RLum`, `RLum.Data`, `plot_RLum`

Examples

```
showClass("RLum.Data.Curve")
```

RLum.Data.Image-class *Class* "RLum.Data.Image"

Description

Class for luminescence image data (TL/OSL/RF).

Objects from the Class

Objects can be created by calls of the form `new("RLum.Data.Image", ...)`.

Slots

`recordType`: Object of class `"character"` containing the type of the curve (e.g. "OSL image", "TL image")

`curveType`: Object of class `"character"` containing curve type, allowed values are `measured` or `predefined`

`data`: Object of class `"RasterBrick"` containing images (raster data).

`info`: Object of class `"list"` containing further meta information objects

`.S3Class`: Object of class `"character"`

Extends

Class `"RLum.Data"`, directly.

Methods

coerce `signature(from = "data.frame", to = "RLum.Data.Image")`
`signature(from = "matrix", to = "RLum.Data.Image")`
Furthermore, lossy coercing is possible from `RLum.Data.Image` to:

`data.frame`, `matrix`

show `signature(object = "RLum.Data.Image")`: ...

set_RLum.Data.Image `signature(recordType = "character", curveType = "character", data = "RasterBr`
Construction method for `RLum.Data.Image` object. The slot `info` is optional and predefined as empty `list` by default.

get_RLum.Data.Image `signature(object = "RLum.Data.Image", info.object = "character")`:
Accessor method for `RLum.Data.Image` object. The argument `info.object` is optional to directly access the info elements. If no info element name is provided, the raw image data (`RasterBrick`) will be returned.

Version

0.1 (2014-07-22)

Note

The class should only contain data for a set of images. For additional elements the slot `info` can be used.

Author(s)

Sebastian Kreutzer, Universite Bordeaux Montaigne (France)

References

#

See Also

`RLum`, `RLum.Data`, `plot_RLum`

Examples

```
showClass("RLum.Data.Image")

##so far no further example available
```

RLum.Data.Spectrum-class
Class "RLum.Data.Spectrum"

Description

Class for luminescence spectra data (TL/OSL/RF).

Objects from the Class

Objects can be created by calls of the form `new("RLum.Data.Spectrum", ...)`.

Slots

`recordType`**:** Object of class `"character"` containing the type of the curve (e.g. "TL" or "OSL")

`curveType`**:** Object of class `"character"` containing curve type, allowed values are `measured` or `predefined`

`data`**:** Object of class `"matrix"` containing spectrum (count) values.

row labels indicating wavelength/pixel values
column labels temperature or time values.

`info`**:** Object of class `"list"` containing further meta information objects

`.S3Class`**:** Object of class `"character"`

Extends

Class "RLum.Data", directly.

Methods

coerce `signature(from = "data.frame", to = "RLum.Data.Spectrum")`
`signature(from = "matrix", to = "RLum.Data.Spectrum")`
Furthermore, lossy coercing is possible from `RLum.Data.Spectrum` to:

`data.frame`, `matrix`

show `signature(object = "RLum.Data.Spectrum")`: ...

set_RLum.Data.Spectrum `signature(recordType = "character", curveType = "character", data = "matri`
Construction method for `RLum.Data.Spectrum` object. The slot `info` is optional and predefined as empty `list` by default.

get_RLum.Data.Spectrum `signature(object = "RLum.Data.Spectrum", info.object = "character")`:
Accessor method for `RLum.Data.Spectrum` object. The argument `info.object` is optional to directly access the info elements. If no info element name is provided, the raw curve data (`matrix`) will be returned.

Version

0.1 (2013-11-23)

Note

The class should only contain data for a single spectra data set. For additional elements the slot `info` can be used.

Author(s)

Sebastian Kreutzer, JLU Giessen (Germany)

References

#

See Also

RLum, RLum.Data, plot_RLum

Examples

```
showClass("RLum.Data.Spectrum")

##show example data (uncomment for usage)
# data(ExampleData.XSYG, envir = environment())
# TL.Spectrum
```

RLum.Results-class *Class* "RLum.Results"

Description

Object class contains results data from functions.

Objects from the Class

Objects can be created by calls of the form `new("RLum.Results", ...)`.

Slots

originator: Object of class "character" containing name of the producing function

data: Object of class "list" containing output data

.S3Class: Object of class "character"

Methods

validObject `signature(object = "RLum.Results")`: validates object depending on the `originator` argument

show `signature(object = "RLum.Results")`: ...

set_RLum.Results `signature(originator = "character", data = "list")`:

Construction method for `RLum.Results` object. The slot `originator` is optional and predefined as the function that calls the function `set_RLum.Results`.

get_RLum.Results `signature(object = "RLum.Results", data.object = "character")`: accessor method for `RLum.Results` object. The argument `data.object` allows directly accessing objects delivered within the slot `data`. If no `data.object` is specified, a preselected object is returned. The default return object depends on the object originator (e.g. `fit_LMCurve`).

merge_RLum.Results `signature(object.list = "list")`: merge method for `RLum.Results` objects. The argument `object.list` requires a list of `RLum.Results` objects.
Merging is done by appending similar elements to the first object of the input list.

Version

0.2.3 (2014-12-16)

Note

The class is intended to store results from functions to be used by other functions. The data in the object should always be accessed by the method `get_RLum.Results`.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France)

References

#

See Also

`RLum`

Examples

```
showClass("RLum.Results")
```

Second2Gray *Converting values from seconds (s) to gray (Gy)*

Description

Conversion of absorbed radiation dose in seconds (s) to the SI unit gray (Gy) including error propagation. Normally used for equivalent dose data.

Usage

```
Second2Gray(data, dose.rate, method = "gaussian")
```

Arguments

data	data.frame (**required**): input values, structure: data (values[,1]) and data error (values [,2]) are required
dose.rate	RLum.Results or vector (**required**): RLum.Results needs to be orginated from the function calc_SourceDoseRate, for vectordose rate in Gy/s and dose rate error in Gy/s
method	character (with default): method used for error calculation (gaussian or absolute), see details for further information

Details

Calculation of De values from seconds (s) to gray (Gy)

$$De[Gy] = De[s] * DoseRate[Gy/s])$$

Provided calculation methods for error calculation: **gaussian** error propagation

$$De.error.gray = \sqrt{(dose.rate * De.error.seconds)^2 + (De.seconds * dose.rate.error)^2))}$$

absolute error propagation

$$De.error.gray = abs(dose.rate * De.error.seconds) + abs(De.seconds * dose.rate.error)$$

Value

Returns a data.frame with converted values.

Function version

0.4 (2015-03-04 13:42:29)

Note

If no or a wrong method is given, the execution of the function is stopped.

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
Michael Dietze, GFZ Potsdam (Germany),
Margret C. Fuchs, AWI Potsdam (Germany),
R Luminescence Package Team

References

#

See Also

#

Examples

```
##(A) for known source dose rate at date of measurement
## - load De data from the example data help file
data(ExampleData.DeValues, envir = environment())
## - convert De(s) to De(Gy)
Second2Gray(ExampleData.DeValues$BT998, c(0.0438,0.0019))
```

```
##(B) for source dose rate calibration data
## - calculate source dose rate first
dose.rate <-  calc_SourceDoseRate(measurement.date = "2012-01-27",
                                  calib.date <- "2014-12-19",
                                  calib.dose.rate <- 0.0438,
                                  calib.error <- 0.0019)
# read example data
data(ExampleData.DeValues, envir = environment())

# apply dose.rate to convert De(s) to De(Gy)
Second2Gray(ExampleData.DeValues$BT998, dose.rate)
```

---

sTeve *sTeve - sophisticated tool for efficient data validation and evaluation*

Description

This function provides a sophisticated routine for comprehensive luminescence dating data analysis.

Usage

```
sTeve (n_frames = 10, t_animation = 2, n.tree = 7, type)
```

Arguments

n_frames	integer (with default): n frames
t_animation	integer (with default): t animation
n.tree	integer (with default): How many trees do you want to cut?
type	integer (optional): Make a decision: 1, 2 or 3

Details

This amazing sophisticated function validates your data seriously.

Value

Validates your data.

Note

This function should not be taken too seriously.

Author(s)

R Luminescence Team, 2012-2013

References

#

See Also

plot_KDE

Examples

```
##no example available
```

---

writeR2BIN *Export Risoe.BINfileData into Risoe BIN-file*

Description

Exports a Risoe.BINfileData object in a *.bin or *.binx file that can be opened by the Analyst software or other Risoe software.

Usage

```
writeR2BIN(object, file, version, txtProgressBar = TRUE)
```

Arguments

object	Risoe.BINfileData (**required**): input object to be stored in a bin file.
file	character (**required**): file name and path of the output file [WIN]: writeR2BIN(object, "C:/Desktop/test.bin"), [MAC/LINUX]: writeR2BIN("/User/test/Desktop/test.bin")
version	character (optional): version number for the output file. If no value is provided the highest version number from the Risoe.BINfileData is taken automatically. Note: This argument can be used to convert BIN-file versions.
txtProgressBar	logical (with default): enables or disables txtProgressBar.

Details

The structure of the exported binary data follows the data structure published in the Appendices of the Analyst manual p. 42.

If LTYPE, DTYPE and LIGHTSOURCE are not of type character, no transformation into numeric values is done.

Value

Write a binary file.

Function version

0.2.5 (2015-03-23 12:57:25)

Note

The function just roughly checks the data structures. The validity of the output data depends on the user.

The validity of the file path is not further checked.
BIN-file conversions using the argument version may be a lossy conversion, depending on the chosen input and output data (e.g., conversion from version 06 to 04 or 03).

Warning

Although the coding was done carefully it seems that the BIN/BINX-files produced by Risoe DA 15/20 TL/OSL readers slightly differ on the byte level. No obvious differences are observed in the METADATA, however, the BIN/BINX-file may not fully compatible, at least not similar to the once directly produced by the Risoe readers!

Author(s)

Sebastian Kreutzer, IRAMAT-CRP2A, Universite Bordeaux Montaigne (France),
R Luminescence Package Team

References

Duller, G., 2007. Analyst.

See Also

readBIN2R, Risoe.BINfileData, writeBin

Examples

```
##uncomment for usage

##data(ExampleData.BINfileData, envir = environment())
##writeR2BIN(CWOSL.SAR.Data, file="[your path]/output.bin")
```

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